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; Sequence 24, Application US/09961400
; Publication No. US20030124131A1
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Best Local Similarity
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Best Local Similarity
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US-09-961-400-24
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SEQ ID NO 24
LENGTH: 110
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US-09-961-400-22
                                                                                                                                                       LENGIH: 117
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APPLICANT: RYBAK, SUSANNA M.
APPLICANT: GOLDENBERG, DAVID M.
APPLICANT: OF UNDENBERG, DAVID M.
TITLE OF INVENTION: INMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
TITLE OF INVENTION: CELLS
TITLE OF INVENTION: US/09/961,400
CURRENT APPLICATION NUMBER: US/09/961,400
                                                                                                       1 MONWATFOOKHIINTPIICNTILDNNIYIVGGOCKRVNTFIISSATTVKAICTGVINLNV 60
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OTHER INFORMATION: catesbeiana ribonuclease with (His) 6 tag, Met at
OTHER INFORMATION: position 7, Met23Leu and Met58Leu substitutions
OTHER INFORMATION: (recombinant Met(-1) RACOR1 Met22Leu Met57Leu-(His)6)
                                                     1 MONWATFOOKHINTPICUTIMDNNIYIVGGOCKRVNTFIISSATTVKAICTGVINMNV
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                                                                                                                                                            61 LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
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  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                   GENEKAL INFORMATION:
APPLICANT: Newton, Dianne L.
APPLICANT: Newton, Dianne L.
APPLICANT: The United States of America
APPLICANT: The United States of America
APPLICANT: as represented by The Secretary of the
APPLICANT: as represented by The Secretary of the
APPLICANT: Department of Health and Human Services
ITILE OF INVENTION: Recombinant Anti-Tumor RNase
FILE REFERENCE: 015280-3431100S
CURRENT APPLICATION NUMBER: US/09/948,391A
CURRENT APPLICATION NUMBER: US 60/079,751
PRIOR APPLICATION NUMBER: W0 PCT/US99/06641
PRIOR FILING DATE: 1998-03-26
PRIOR FILING DATE: 1998-03-26
PRIOR FILING DATE: 2000-08-17
NUMBER: OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2: SEQ ID NOS: 43
LENGTH: 117
  0;
  2; Mismatches
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PRIOR FILING DATE: 2000-08-17
PRIOR APPLICATION NUMBER: PCT/US99/06641
                                                                                                                                                                                                                                                                                                                         US-09-948-391A-22

Sequence 22, Application US/09948391A

; Publication No. US20030027311A1

; GENERAL INFORMATION:
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  109; Conservative
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i US-09-948-391A-24

i Sequence 24, Application US/09948391A

j Publication No. US20030027311A1

GENERAL INFORMATION:

APPLICANT: Pybak, Susanna M.

APPLICANT: Newton, Dianne L.

APPLICANT: The United States of America

APPLICANT: The United States of America

APPLICANT: Department of Health and Human Services

TITLE OF INVENTION: Recombinant Anti-Tumor RNase

FILE REFERENCE: 015280-343110US

CURRENT APPLICANTION NUMBER: US 60/079,751

PRIOR PILING DATE: 2002-05-10

PRIOR APPLICATION NUMBER: US 60/079,751

PRIOR APPLICATION NUMBER: WO PCT/US99/06641

PRIOR FILING DATE: 1998-03-26

PRIOR FILING DATE: 2000-08-17

NUMBER OF SEQ ID NOS: 43

SOFTWARE: PatentIn Ver. 2.0
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100.0%; Pred. No. 3.1e-60;
tive 0; Mismatches 0;
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Pred. No. 1.2e-60;
2; Mismatches 0;
PRIOR FILING DATE: 1999-03-26
PRIOR APPLICATION NUMBER: 60/079,751
PRIOR FILING DATE: 1998-03-26
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 22
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ORGANISM: Artificial Sequence
FEATURE:
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98.2%;
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Pred. No. 8.5e-61;
0; Mismatches 1;
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99.1%; Pred. No. 1.1e-60;
tive 0; Mismatches 1;
## PRIOR FILING DATE: 2000-08-17
| PRIOR APPLICATION NUMBER: PCT/US99/06641
| PRIOR APPLICATION NUMBER: 60/079,751
| PRIOR FILING DATE: 1998-03-26
| NUMBER OF SEQ ID NOS: 43
| SEQ ID NO 26
| LENGTH: 111
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                                                                                                                                                                                   Query Match
Best Local Similarity 99.15
Matches 110; Conservative
                                                                                                                                            ORGANISM: Rana catesbeiana
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Best Local Similarity 99.1
Matches 110; Conservative
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RESULT 7 US-09-948-391A-21

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Sequence 21, Application US/09961400
| Publication No. US20030124131A1
| GENERAL INFORMATION:
| APPLICANT: RESERVE, SUSANNA M. |
| APPLICANT: GOLDENBERG, DAVID M. |
| APPLICANT: GOLDENBERG, DAVID M. |
| APPLICANT: GOLDENBERG, DAVID M. |
| APPLICANT: METON: INFUNCONUUGATES OF TOXINS DIRECTED AGAINST MALIGNANT: TITLE OF INVENTION: INMUNOCONUUGATES OF TOXINS DIRECTED AGAINST MALIGNANT |
| TITLE OF INVENTION: CELLS |
| TILLE OF INVENTION: ONBER: US/09/961,400 |
| TILLE OF INLING DATE: 2001-09-25 |
| FILE REFERENCE: 2001-09-25 |
| RIOR APPLICATION NUMBER: 09/622,613 |
| PRIOR APPLICATION NUMBER: PCT/US99/06641 |
| PRIOR PILING DATE: 1999-03-26 |
| PRIOR FILING DATE: 1999-03-26 |
| NUMBER OF SEQ ID NOS: 43 |
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                                                                                                                 APPLICANT: Nyac, Sugarda n., APPLICANT: Newton, Dianne L., APPLICANT: The United States of America APPLICANT: The United States of America APPLICANT: The United States of America APPLICANT: as represented by The Secretary of the APPLICANT: Department of Health and Human Services TITES OF INVENTION: Recombinant Anti-Tumor RNase FILE REFERENCE: 015280-34311005 / 948,391A CURRENT APPLICATION NUMBER: US 60/079,751 PRIOR APPLICATION NUMBER: US 60/079,751 PRIOR FILING DATE: 1998-03-27 PRIOR FILING DATE: 1998-03-27 PRIOR FILING DATE: 1998-03-26 PRIOR FILING DATE: 2000-08-17 NUMBER: OF SEQ ID NOS: 43 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 21
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Pred. No. 1.1e-60;
US20030027311A1
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ORGANISM: Artificial Sequence
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98.2%;
                                                                                        APPLICANT: Rybak, Susanna M.
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Matches 109; Conservative
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ORGANISM: Rana catesbeiana
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                                       GENERAL INFORMATION:
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APPLICANT: RYBAK, SUSANNA M.
APPLICANT: GOLDENBERG, DAVID M.
APPLICANT: GOLDENBERG, DAVID M.
APPLICANT: NEWTON, DIANNE L.
TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT TITLE OF INVENTION: CELLS
FILE REFERENCE: 018733/1059
CURRENT FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: 09/622,613
PRIOR PILING DATE: 1999-03-26
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 1998-03-26
NUMBER OF SEQ ID NOS: 43

SOFTWARE PARCHAIN VOR: 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Description of Artificial Sequence:Rana OTHER INFORMATION: catesbeiana cocyte ribonuclease (RaCOR1) synth OTHER INFORMATION: gene modified to use E. coli preferred codons
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62 STTREQLATCTRISITPRPCPYSSRIETNYICVKCENQYPVHFAGIGRCP 111
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99.2%; Score 602; DB 10; Length 110;
Best Local Similarity 100.0%; Pred. No. 8.4e-61;
Matches 110; Conservative 0; Mismatches 0; Indels (
                                                                           Sequence 15. Application US/09948391A

Publication No. US20030027311A1

GENERAL INFORMATION:
APPLICANT: Rybar Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: The United States of America
APPLICANT: as represented by The Secretary of the APPLICANT: Department of Health and Human Services;
TITLE OF INVENTION: Recombinant Anti-Tumor RNase;
FILE REFERENCE: 015280-343110US

CURRENT FILING DATE: 2002-05-10
                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 60/079,751
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: WO PCT/US99/06641
PRIOR APPLICATION NUMBER: WO PCT/US99/06641
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 2000-08-17
NUMBER OF SEQ ID NOS: 43
SOFTHARE: PALENTIN Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Artificial Sequence
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APPLICANT: GOLDENBERG, DAVID M.
APPLICANT: GOLDENBERG, DAVID M.
TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
TITLE OF INVENTION: CELLS
TITLE OF INVENTION: CELLS
                                                                                                                                                                                                                                                               1 ONWAIFQOKHIINTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNVL 60
                                                                                                                                                                                         2 QNWATFQQKHIINTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNVL
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             Length 110;
                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Nyaer, Sugainary, Applicant in APPLICANT: Newton, Dianne I., APPLICANT: The United States of America APPLICANT: The United States of America APPLICANT: as represented by The Secretary of the APPLICANT: Department of Health and Human Services TITLE OF INVENTION: Recombinant Anti-Tumor RNase TITLE OF INVENTION: NOWBER: US/09/948,391A CURRENT APPLICATION NUMBER: US 60/079,751 PRIOR APPLICATION NUMBER: US 60/079,751 PRIOR APPLICATION NUMBER: WS 60/079,751 PRIOR PILING DATE: 1999-03-26 PRIOR FILING DATE: 1999-03-26 PRIOR FILING DATE: 2000-08-17 NUMBER: OS SEQ ID NOS: 43 SEQ ID NO SEQ ID NOS: 43 SEQ ID NO SEC ID NO SEC ID NOS: 43 SEQ ID NO SEC ID NOS: 43 SEQ ID NOS: 4
                           Score 602; DB 10;
Pred. No. 8.4e-61;
99.2%; Sco. 100.0%; Pred. No. v. ... 0; Mismatches
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CURRENT APPLICATION NUMBER: US/09/961,400
CURRENT FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: 09/622,613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 26, Application US/09948391A Publication No. US20030027311A1 GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Rybak, Susanna M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 99.1
Matches 110; Conservative
                                                                                                                        110; Conservative
                                                                          Similarity
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US-09-961-400-26
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US-09-948-391A-26
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Мау Run on:

7, 2004, 21:29:40 ; Search time 35.6155 Seconds (without alignments) 865.070 Million cell updates/sec

US-09-961-400-17

Perfect score:

1 MQNWATFQQKHIINTPIICN......ICVKCENQYPVHFAGIGRCP 111 Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

1140673 seqs, 277566755 residues Searched:

Total number of hits satisfying chosen parameters: seq length: 0
seq length: 2000000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Published Applications AA:*

1: \cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*

2: \cgn2_6/ptodata/2/pubpaa/PCT NEW PUB.pep:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	Description	1 1	, , ,	15,	Sequence 15, Appl	76,	76,	Sequence 17, Appl	, [6	1 .	77	22,	Sequence 22, Appl			#7	sequence 19, Appl	Sequence 19, Ann	6, A	
SUMMARIES	di.	US-09-961-400-17	US-09-948-391A-15	IIS-09-961-400-15	TIS-09-940-2018	TIS-09-961 400 20	170 - 00 - 00 - 00 - 00 - 01 - 10 - 00 -	/ T-WT65-946-60-60	US-09-948-391A-21	US-09-961-400-21	118-09-948-3917-33	TE-00 001 400 00	77-004-196-60-60	US-09-948-391A-24	US-09-961-400-24	TIS-09-961-400-19	TION TO 00 01	02-03-348-39LA-19	US-09-948-391A-6	
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e)e	Query Match	100.0	99.2	99.2	99.2	99.2	0.66		2,5	99.0	0.66	0.66			78. A	98.2	67.2	1 .	7.7	
	Score	607	602	602	602	602	601	103	100	601	601	601	707	100	1.60	596	290		6.007	
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	14 US-10-153-882-2 10 US-09-961-400-2	-60-SD	-09-961-	US-09-948	10 US-09-961-400-28			10 US-09-948-391A-11	10 US-09-961-400-11	10 US-09-948-391A-4	10 US-09-967-400-4	200	ו מ	IIS-09-948-391		12 IIS-10-461-713-52	TIS-09-986-119-3	- CII	118-10-016-447		12 IIS-10-016-248-89		10 10 01 010 01 10 10 10 10 10 10 10 10		:	05-09-731-872-25	-166-918-60-SD 0	9 US-09-981-286A-8
105 111	105	105	105	127	127	104	105	104	104	104	104	104	104	105	111	104	83	83	169	124	119	119	σ	124	177	, r	14/	124
47.2	46.5	46.4	46.4	46.4	46.4	46.2	46.2	45.6	45.6	45.4	45.4	44.9	44.9	44.7	44.7	44.4	33.9	33.9	26.9	22.3	21.7	21.7						ν. Σ
286.5	282.5	281.5	281.5	281.5	281.5	280.5	280.5	276.5	276.5	275.5	275.5	272.5	272.5	271.5	271.5	269.5	206	206	163	135.5	131.5	131.5	121	117.5	117	117	1 7 7 7	114.5
116	13	20	21	22	23	24	25	56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	4	44) F

ALIGNMENTS

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Sequence 17, Application US/09961400
Sequence 17, Application US/09961400
Sequence 17, Application No. US20030124131A1
Septiman No. US20030124131A1
SERENATI INPORMATION:
APPLICANT: RYBAK, SUSANNA M.
APPLICANT: GOLDENBERG, DAVID M.
TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
TITLE OF INVENTION: CELLS
TITLE OF INVENTION: UNMERR. US/09/961,400
CURRENT APPLICATION NUMBER: 09/622,613
FRIOR PEPLICATION NUMBER: 09/622,613
FRIOR PEPLICATION NUMBER: 09/622,613
FRIOR APPLICATION NUMBER: 60/079,751
FRIOR APPLICATION NUMBER: 60/079,751
FRIOR APPLICATION NUMBER: 60/079,751
SPRIOR APPLICATION NUMBER: 60/079,751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 607; DB 10; Length 111; 100.0%; Pred. No. 2.3e-61; ative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Rana catesbeiana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 111; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
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61 LSTTRFQLNTCTRISITPRPCPYSSRIETNYICVKCENQYPVHFAGIGRCP 111 LSTTRFQLNTCTRTSITPRFCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NVLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
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45.7%; Score 277.5; DB 3; Length 254;
Best Local Similarity 49.1%; Pred. No. 2.2e-24;
Matches 55; Conservative 15; Mismatches 33; Indels 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 49, Application US/08875811

Sequence 19, Application US/08875811

Sequence 10. 6045733

GRNERAL INFORMATION:

APPLICANT: Ryback, Susanna M.

APPLICANT: Boque, Lluis

APPLICANT: Widawer, Alexander

TITLE OF INVENTION: Recombinant Ribonuclease Proteins

NUMBER OF SEQUENCES: 64

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: PAPLICATION NUMBER: US/08/875,811 FILING DATE: US-FEB-1998 CLASSIFICATION: 435
                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco STATE: California COUNTRY: USA ZIP: 94111-3834
                                                                                                                                                                                                    PRIOR ASSISTATION 1333
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
FILING DATE: 19-FEB-1996
APPLICATION NUMBER: US 60/011,800
APPLICATION NUMBER: US 60/011,800
APTORNEY/AGENT INFORMATION:
NAME: Faris, Susan K.
REGISTRAINON NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 015280-244100US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                               015280-244100US
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APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 254 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , MOLECULE TYPE: protein US-08-875-811-61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
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US-08-875-811-49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26 QDWLTFQKKHITNTRDVDCDNIMSTNLF----HCKDKNTFIYSRPEPVKALCKGIIASKN
59 NVLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
                        64 NVLTTSEFYLSDC---NVTSRPCKYKLKKSTNKECVTCENQAPVHFVGVGSC 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VLTTSEFYLSDC---NVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        45.7%; Score 277.5; DB 3; Length 129; 49.5%; Pred. No. 9.6e-25;
                                                                                                                                              Sequence 63, Application US/08875811
; Sequence 63, Application US/08875811
; Patent No. 6045793
; GENERAL INFORMATION:
APPLICANT: Rybak, Susanna M.
APPLICANT: Rybak, Lluis
APPLICANT: Wlodawer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
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PATENTIN NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
CLASSIFTCATION NUMBER: WC/08/875,811
FILING DATE: 19-FEB-1998
CLASSIFTCATION DATA:
APPLICATION NUMBER: WC PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Faris, Susan K.
REFERENCE/DOCKET NUMBER: 015280-244100US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 59, Application US/08875811
Patent No. 6045793
GENERAL INFORMATION:
APPLICANT: RYDAK, Susanna M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : 129 amino acids
amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 94111-3834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 13
US-08-875-811-59
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1 MONWATEQOKHIINT-PIICNTIMDNNIYIVGGOCKRVNTFIISSATTVKAICTGVI-NM 58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 45.7%; Score 277.5; DB 3; Length 3 Best Local Similarity 49.1%; Pred. No. 2.2e-24; Matches 55; Conservative 15; Mismatches 33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 61, Application US/08875811

Patent No. 6045793

GENERAL INFORMATION:
APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: Modawer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
APPLICANT: Newton, Dianne L.
APPLICANT: Boque, Lluis
APPLICANT: Wlodawer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                   OPERATION SYSTEM: PC-DCS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,811 FILING DATE: 19-FEB-1998 CLASSIFICATION DATE: 875 FILING APPLICATION DATE: 997 PRIOR APPLICATION DATE: 997 PRIOR APPLICATION NUMBER: WG 60/011,800 FILING DATE: 19-FEB-1997 PRIOR APPLICATION NUMBER: US 60/011,800 FILING DATE: 21-FEB-1996 ATTONEY/AGENT INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco STATE: California
                                                                                                                          SSEE: Townsend and Townsend and Crew LLP
F: Two Embarcadero Center, Eighth Floor
San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Faris, Susan K.
REGISTRATION NUMBER: 41,739
REFERENCE DOCKET NUMBER: 015280-244100US
TELECOMMUNICATION INPORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : 251 amino acids
amino acid
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
                                                                                                                                                                                                                      California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Y: USA
94111-3834
                                                                                                                                                                                                                                                                 ZIP: 94111-3834
                                                                                                                                                ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-875-811-61
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                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                            STREET:
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9; Gaps

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2 QNWATFQQKHIINT-PIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NMN 59
                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MQNWATFQQKHIINT-PIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENOYPVHFAGIGRC 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6
                                                                                                                                                                                                                                                Length 104;
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49.1%; Pred. No. 8.1e-25;
tive 15; Mismatches 33; Indels 9
                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: Boque, Lluis
APPLICANT: Woldawer, Alexander
TITLE OF INVENTIONS: 64
NUMBER OF SEQUENCES: 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPRAING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02588
FILING APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: FAZIS: SUSAN K.
REGISTRATION NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 015280-244100US
TELECOMMUNICATION INFORMATION:
MATCHEROMATICATION NUMBER: 015280-244100US
                                                                                                                                                                                                                                        DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SSEE: Townsend and Townsend and Crew LLP
[: Two Embarcadero Center, Eighth Floor
San Francisco
                                                                                                                                                                                                                            Query Match
45.7%; Score 277.5; DB 4
Best Local Similarity 49.5%; Pred. No. 7.4e-25;
Matches 55; Conservative 15; Mismatches 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 32, Application US/08875811 Patent No. 6045793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (415) 576-0200
TELERAX: (415) 576-0300
INFORMATION FOR SEG ID NO: 32:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               112 amino acids
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Best Local Similarity 49.19
Matches 55; Conservative
                                                                        ; TOPOLOGY: linear; MOLECULE TYPE: protein US-09-095-429-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein US-08-875-811-32
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
GY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 11
US-08-875-811-32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Mâtch 45.7%; Score 277.5; DB 4;
Best Local Similarity 49.5%; Pred. No. 7.4e-25;
Matches 55; Conservative 15; Mismatches 32;
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/095,429
                                                                                                                                                    REFERENCE DOCKET NUMBER: 15280-267
TELEPONNUNICATION INFORMATION: TELEFAX: (415) 543-5060
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHRACTERISTICS: LENGTH: 104 amino acids
TYPE: amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15280-267
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FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Ran, David B.
REGISTRATION VIMBER: 38,589
REFERENCE/DOCKET NUMBER: 15280
TELEPHONE: (415) 543-9600:
TELEPAX: (415) 543-9600:
TELEPAX: (415) 543-9600:
TELEPAX: (415) 543-9600:
TELEPAX: (415) 643-9600:
TELEPAX: (415
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/626,288
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Ran, David B.
REGISTRATION NUMBER: 38,589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; MOLECULE TYPE: protein US-08-626-288-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
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Gaps

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GENERAL INFORMATION:
GENERAL GENERAL STATES
GENERAL SPETICATION NUMBER:
GURRENT FILING DATE:
FRIOR APPLICATION NUMBER:
FRIOR FILING DATE:
FRIOR FILING DA
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                                                                                                                                                           |:| |||:||| || : |: || |:: |
| QDWLIFQKKHITNIRDVDCDNIMSTNLF----HCKDKNTFIYSRPEPVKALCKGIIASKN 56
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                                                                                                                                                                                                                                                   60 VLSTTRFQLNTCTRISITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
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APPLICANT: Youle, Richard
APPLICANT: Youle, Richard
APPLICANT: Win, Youn-Neng
APPLICANT: Win, Youn-Neng
APPLICANT: Boix, Ester
APPLICANT: Ardelt, Wojeiech
TITLE OF INVENTION: A Mutant Form of Cytotoxic Protein Which
TITLE OF INVENTION: A Mutant Production by Recombinant Methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 45.7%; Score 277.5; DB 4; Length 104;
49.5%; Pred. No. 7.4e-25;
tive 15; Mismatches 32; Indels 9;
Pred. No. 7.4e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 94105-14>c
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/626,288
TIING DATE: No. 6649392 yet assigned
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ADDRESSEE: Townsend and Townsend and Crew
                                                            15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/08626288
Patent No. 6649392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/09687748 Patent No. 6423515
                                 49.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55; Conservative
                                                                Conservative
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California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Rana pipiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                              Best Local Similarity
Matches 55; Conserv
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STATE: Ca
COUNTRY:
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TITLE OF INVENTION: NUCLEIC ACIDS ENCODING RIBONUCLEASES AND METHODS OF
TITLE OF INVENTION: NUCLEIC ACIDS
FILE REPERENCE: 5013
CURRENT APPLICATION NUMBER: US/09/394,268
CURRENT FILING DATE: 1999-09-10
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 104
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                                 APPLICANT: Wlodawer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Bighth Floor
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 46.0%; Score 279.5; DB 3; Best Local Similarity 49.1%; Pred. No. 2e-24; Matches 55; Conservative 16; Mismatches 32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
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NFR: 015280-244100US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 19-FEB-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OORPHTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Faris, Susan K.
REGISTRATION UNDHER: 41,739
REPERENCE/DOCKET NUMBER: 01528
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  45.78;
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amino acid
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; ORGANISM: Rana pipiens
US-09-394-268-1
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94111-3834
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Query Match

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1 MONWATEQOKHIINT-PIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NM 58
               59 NVLSTTRFQLNTCTRISITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
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                                                                                                                                                              APPLICANT: Rybak, Susanna M.
APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: Newton, Dianne L.
APPLICANT: Hoddwer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STREET: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
APPLICATION DUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       46.0%; Score 279.5; DB 3;
49.1%; Pred. No. 1.9e-24;
Live 16; Mismatches 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PULING APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Paris, Susan K.
RECISTRATION NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 015280-244100US
                                                                                                                               Sequence 41, Application US/08875811
Patent No. 6045793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 51, Application US/08875811; Patent No. 6045793; GENERAL INFORMATION: APPLICANT: Rybak, Susanna M. APPLICANT: Newton, Dianne L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             355 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Newton, Dianne
Boque, Lluis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 49.18
Matches 55; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                94111-3834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                                                                                                                                USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE:
                                                                                        RESULT 5
US-08-875-811-41
                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-875-811-41
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                                     57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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                                                                                                                                                         1 MONWATFOOKHIINT-PIICNTIMDNNIYIVGGOCKRVNTFIISSATTVKAICTGVI-NM 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDWLTFQKKHITNTRDVDCDNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASK 56
                                                                                                                               2 QNWATEQOKHIINT-PIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NNN
                                                                                                         Gaps
                                                                                                                                                                                                        60 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENOYPVHFAGIGRC 110
                                                                                                                                                                                                                               59 NVLSTTRFQLNTCTRISITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
                                                                                                        9;
                                                              DB 1; Length 104;
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                                                                                                    31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   46.0%; Score 279.5; DB 3; Length : 49.1%; Pred. No. 4.4e-25; Live 16; Mismatches 32; Indels
                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: Boque, Lluis
APPLICANT: WIddawer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Bighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 94111-4854

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OFBRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Parentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
                                                      46.9%; Score 284.5; DB 1
49.5%; Pred. No. 1.1e-25;
Live 16; Mismatches 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PULICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTOKNEY/ARENT INFORMATION:
REGISTRATION NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 015280-244100US
TELECOMMUNICATION INFORMATION:
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Patent No. 6045793
GENERAL INFORMATION:
   Oocyte
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TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
                                           Query Match
Best Local Similarity 49.58
Matches 55, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         105 amino acids
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Best Local Similarity 49.1%
Matches 55; Conservative
; DEVELOPMENTAL STAGE:
US-08-467-955-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; MOLECULE TYPE: protein US-08-875-811-39
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STATE: California
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Gaps

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ORGANISM: Rana pipiens
    ) OTHER INFORMATION:
) OTHER INFORMATION:
US-08-875-811-8
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                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                           61 LSTTRFQLNTCTRISITPRPCPYSSRIETNYICVKCENQYFVHFAGIGRCP 111
                                                                                                                                                                                                                                                                                                                                                                                      61 LSTTREQLNTCTRISITERPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
                                                                                                                                                                                                                                                            1;
                                                                                                                                                                                                                 Length 111;
                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 8, Application US/08875811
Patent No. 6045793
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Newton, Dianne L.
APPLICANT: Newton, Dianne L.
APPLICANT: Hoddwer, Lluis
APPLICANT: Hoddwer, Alexander
TITLE OF INTENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
                                                                                LOCATION: 1..111
; OTHER INFORMATION: /note= "Frog Lectin from Rana;
; OTHER INFORMATION: catesbeiana"
US-08-891-848-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30
CUBRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
                                                                                                                                                                                                                 Query Match 97.0%; Score 588.5; DB 2; Best Local Similarity 98.2%; Pred. No. 6.6e-61; Matches 109; Conservative 1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                015280-244100US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WS 60/011,800
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Faris, Susan K.
REGISTRATION NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 015280-244100US
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Paine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : 111 amino acids
amino acid
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LENGTH: 111 amino acidi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: protein
                                               MOLECULE TYPE: protein
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STRANDEDNESS:
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US-08-875-811-8
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2 QNWATFQQKHIINTPII-CNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNV 60
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; Sequence 2, Application US/08467955
; Fatent No. 572804
; GENERAL INFORMATION:
    APPLICANT: Ardelt Ph.D, Wojciech J.
    APPLICANT: Ardelt Ph.D, Wojciech J.
    APPRICANT: Ardelt Ph.D, Wojciech J.
    APPRESSES: 2
    CORRESPONDENCE ADDRESS: 2
    CORRESPONDENCE ADDRESS: 3
    ADDRESSES: Mark H. Jay, P.A.
    STREET: P.O. Box E
    CITY: Short Hills
    STATE: New Jersey
                                                                                                                                                                                                                                                                                                     61 LSTTREQLNTCTRISITPRECPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
                                                                                                                                                                                                                                                                                                                               61 LSTTREQLNTCTRISTTERECEYSSRIETNYICVKCENQYPVHFAGIGRCP 111
                                                                                                Score 588.5; DB 3; Length 111;
Pred. No. 6.6e-61;
1; Mismatches 0; Indels 1
/note= "Frog Lectin from Rana
catesbeiana"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/178,118
FILING DATE: 06-APR-1988
FRICK APPLICATION DATA:
APPLICATION NUMBER: US 07/436,141
FILING DATE: 13-NOV-1989
FRICK APPLICATION NUMBER: US 07/814,332
FILING DATE: 03-FEB-1992
FRICK APPLICATION DATA:
APPLICATION NUMBER: US 07/814,332
FILING DATE: 01-ABS-1992
APLICATION NUMBER: US 07/814,332
APLICATION NUMBER: US 08/283,970
FILING DATE: 01-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk COMPUTER: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFFWARE: Patentin Release #1.24 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/467,955 FILING DATE:
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TELEX: No. 5728805 Applicable
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 27507
REFERENCE/DOCKET NUMBER: 50
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-912-9066
                                                                                                        97.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       104 amino acids
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                                                                                                        Query Match
Best Local Similarity 98.23
Matches 109; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein HYPOTHETICAL: N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 07078-0383
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Jay, Mark H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
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ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ANTI-SENSE: N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
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11, Appli 26, Appli 30, Appli 24, Appli 2, Appli 2, Appli 45, Appli 53, Appli 33, Appli 34, Appli 47, Appli 48, Appli 47, Appl

Sat

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13, Appl
1, Appli
2, Appli
1, Appli
2, Appli
2, Appli
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1, Appli
1, Appli
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Sequence 8, Appli
                                                                                                                                                                       / Search time 12.8756 Seconds
(without alignments)
445.066 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Ag
Sequence 39, A
Sequence 51, A
Sequence 1, A
Sequence 23, A
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                                                                                                                                                                                                                                                                                                                                                   1 MQNWATFQQKHIINTPIICN.....ICVKCENQYPVHFAGIGRCP
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Sequence 3
Sequence 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Issued Patents AA:*

1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
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5: /cgn2_6/ptodata/2/iaa/PcTUS_COMB.pep:*
GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-891-848-12
US-08-875-811-8
US-08-875-811-8
US-08-875-811-31
US-08-875-811-31
US-09-687-748-1
US-09-687-748-1
US-09-095-811-32
US-09-095-811-32
US-08-875-811-63
US-08-875-811-63
US-08-875-811-63
US-08-875-811-64
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Listing first 45 summaries
                                                                                                               protein search, using sw model
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1005 1006 1006 1006 1007 1007 1007 1007 1007	usanna h Lichard i Lichard i Lichard i Selecti Selecti Selecti SS: nd and 7 compatib PC-DOS/ In Releas DATA: EP-1993 IN 120 08 IN 120 00 IN 120 08 IN 120 00 IN 120 00
4 4 4 4 4 4 4 4 4 4 4 8 8 8 7 7 7 7 8 8 8 7 7 7 7	12, Application 0. 5955073 INCRMATION: CANT: Rybak, Su. CANT: Rybak, Su. CANT: Rybak, Su. CANT: Newton, D. CANT: Newton, D. CANT: Nicholls, OF INVENTION: SR OF SEQUENCES: SPONDENCE ADDRES, SPONDENCE ADDRES, SPONDENCE ADDRES, SPONDENCE ADDRES, SPONDENCE ADDRESS, SPONDENCE ADDRESS, SPONDENCE ADDRESS, SPONDENCE ADDRESS, SPONDENCE ADDRESS, ING DATE: Two Embarce ING DATE: 1BM PC CC, MATING SYSTEM: 1BM PC CC, MATING SYSTEM: 1MG DATE, ICATION NUMBER: 1MG DATE, ICATION NUMBER: NG DATE, ICATION NUMBER: NG DATE: 22-OGT APPLICATION NUMBER: NG DATE: 1CATION NUMBER: 1CATIO
232.5 2225 235 235 235 235 235 235 235 235 2	SGULT 1 S-08-891-848-12 Sequence 12, Applicat Patent No. 5955073 GENERAL INFORMATION: APPLICANT: Rybak, APPLICANT: Rybak, APPLICANT: Nybak, APPLICANT: Nichol TITLE OF INVENTION NUMBER OF SEQUENCE CORRESPONDENCE ADD ADDRESSEE: Two End STREET: Two End STREET: Two End STREET: Two End CUTY: San Franc STATE: ADILIFORM OF SEQUENCE COMPUTER: 1BM POUNTRY: USA ZIP: 94111-3834 COMPUTER: 1BM POURTAING SYSTEM SOFTWARE: PATENT OF COMPUTER: 1BM POPERATION IN PAPLICATION IN APPLICATION IN REFERENCE/DOCKET TELECOMMUTICATION IN REFERENCE/DOCKET TELEFAX: (415) 5 INFORMATION FOR SEQ ISSECTION OF CHARACTERIAL LENGTH: 111 aminn TYPE: aminn acidd
GG G E E E E E E E E E E E E E E E E E	RESULT 1 US-08-891- Sequence Patent APPLI

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AAW35115 to AAW35123 encode recombinant proteins (rOnc) which are modifications of the RNase Onconase (RTM) (nOnc). Such novel ribonuclease modifications are highly cytotoxic and can be used alone or to form chemical conjugates or to target recombinant immunofusions. They are used particularly for decreasing tumour cell growth. They can also be used for cell separation in vitro by selectively killing unwanted types of cells,
                                                                                                                                                                                                                                                                                                                                                                                                                                                              e.g. in bone marrow prior to transplantation into a patient undergoing marrow ablation by radiation, or for killing leukaemia cells or T-cells that would cause graft versus host disease. The toxins can also be used to selectively kill unwanted cells in culture. The new ribonucleases have increased cytotoxic activity compared to none and also lower
                                                                                                                                                                                                                                                                                  Ribonuclease molecules based on native Onconase
                                                                                                                                                                 (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                  Disclosure, Page 65-66, 90pp; English.
                                                                                                                                                                                                                                                                                                     particularly tumour cells.
                                                                                                                                                                                                                                                  N-PSDB; AAT94959
   Rana pipiens.
                                    WO9731116-A2
                                                                                                 19-FEB-1997;
                                                                                                                                    21-FEB-1996;
                                                                    28-AUG-1997.
                                                                                                                                                                                                   Rybak SM,
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Job time
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence is a Rana pipiens Clone 5alb ribonuclease (RaPLRI). It is encoded by Clone 5alb cDNA obtained from Rana pipiens liver mRNA library. It exhibits differences with Oncoase (RTM) at amino acid residues 11, 20, 85 and 103. Carboxy terminal end of RaPLRI has a covalently bound ligand binding moiety, which can be a LL2 antibody directed against CD22 on cancerous B cells or human charionic gonadotrophin (hGG) effective against Kaposi's Sarcoma cells. Recombinant ribonucleases can be expressed in bacteria without an N-terminal methionine due to the presence of a signal peptide that is cleaved by bacteria. The soluble expression of ribonuclease allows the proteins to be fused in-frame with ligand binding moieties to form cytocloxic fusion proteins. They can be used for treatment of cancer and autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 QNWATFQQKHIINT-PIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NMN 59
                                                                                                                                                                                                                                                                                                                                                                                                                          New recombinant ribonucleases, used for killing target cells, e.g. for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24 QDWLTFQKKHLTNTRDVDCNNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            46.4%; Score 281.5; DB 2; Length 127; 49.5%; Pred. No. 3.7e-24; live 15; Mismatches 32; Indels 9
                                                                                                                                                /label= Rana_pipiens_Clone_5alb_ribonuclease
                                                                                                                                                                                                                                                                                                                                                                                                                                                treating cancers, viral infections or autoimmune diseases
                                                                             1. .23
/label= Signal_peptide
/note= "Putative"
24. .127
                                                                                                                                                                                                                                                                                                            (USSH ) US DEPT HEALTH & HUMAN SERVICES
                                                                 ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 69; 71pp; English
                                                                                                                                                                                                                                              99WO-US006641
                                                                                                                                                                                                                                                                               98US-0079751P
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es 55; Conservative
                                                                                                                                                                                                                                                                                                                                              Newton DL;
                                                                                                                                                                                                                                                                                                                                                                           WPI; 1999-610847/52.
N-PSDB; AAZ08136.
 autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 127 AA;
                                                                                                                                                                                                                                                                             27-MAR-1998;
                                Rana pipiens
                                                                                                                                                                             WO9950398-A2
                                                                                                                                                                                                               07-0CT~1999
                                                                                                                                                                                                                                                                                                                                             Rybak SM,
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                                                                 Key
Peptide
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- used for killing cells,

Wlodawer A;

Boque L,

Newton DL, 1997-435168/40.

97WO-US002588 96US-0011800P.

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1 MONWATFOOKHIINT-PIICNTIMDNNIYIVGGOCKRVNTFIISSATTVKAICTGVI-NM
                                                                                                          9; Gaps
                                                                                                                                                                                                             59 NVLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
                                                                                                                                                                                                                                    Length 105;
                                                                                                          Indels
                                                                 46.0%; Score 279.5; DB 2;
49.1%; Pred. No. 5e-24;
live 16; Mismatches 32;
                                                                                                                                                                                                                                                                                                     7, 2004, 21:38:28
                                                                 Query Match
Best Local Similarity 49.1%
Matches 55, Conservative
immunogenicity in humans
                                                                                                                                                                                                                                                                                                    completed: May 1e : 47.3489 secs
                                   Sequence 105 AA;
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RNase A; ribonuclease; cytotoxic; onconase; nOnc; immunofusion; tumour cell growth; frog.

R. pipiens recombinant RNase protein [Met-(-1)]rOnc.

(first entry)

20-APR-1998

AAW35123 ID AAW3 XX AC AAW3 XX ZO-P XX XX E. F XX XX RNAE KW RNAE XX XW TUMK XX

AAW35123;

AAW35123 standard; protein; 105 AA.

RESULT 15

recombinant ribonuclease; cytotoxic fusion protein; cancer; frog;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QNWATFQQKHIINT-PIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NMN 59
                                                                                                                 LL2 antibody;
                                                                                                            Rana pipiens liver ribonuclease, RaPLRI; covalently bound; LL2 antibody ligand binding moiety, CD22; cancerous B cell; Kaposi's Sarcoma; frog; human chorionic gonadotrophin; hCG; recombinant ribonuclease; RNase; signal peptide; cytotoxic fusion protein; cancer; autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QDWLTFQKKHLTNTRDVDCNNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New recombinant ribonucleases, used for killing target cells, e.g. treating cancers, viral infections or autoimmune diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        46.4%; Score 281.5; DB 2; Length 104; 49.5%; Pred. No. 2.9e-24; tive 15; Mismatches 32; Indels 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Recombinant Met(-1) RaPLR1 Gln1Ser amino acid sequence.
                                                                              Rana pipiens liver ribonuclease (RaPLR1).
                                                                                                                                                                                                                                                                                                                                                             (USSH ) US DEPT HEALTH & HUMAN SERVICES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 55; 71pp; English.
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                                                                                                                                                                                                                                                                                                     99WO-US006641.
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                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         55; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1999-610847/52.
                                                                                                 kana pipiens liver
ligand bindir
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 104 AA;
                                                                                                                                                                                                                                                                                                  26-MAR-1999;
                                                                                                                                                                                                                                                                                                                                 27-MAR-1998;
                                                                                                                                                                                                 Rana pipiens
                                                                                                                                                                                                                                 WO9950398-A2
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             AAY28865;
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The present sequence is a recombinant Rana pipiens ribonuclease (RaPLRI) protein with Met at position 1 and Gln2Ser. Carboxy terminal end of recombinant RaPLRI has a covalently bound ligand binding moiety, which can be a LL2 antibody directed against CD22 on cancerous B cells or human chorionic gonadotrophin (hGG) effective against Kaposi's sarcoma cells. Recombinant ribonucleases can be expressed in bacteria without an N-reminal methionine due to the presence of a signal peptide that is cleaved by bacteria. The soluble expression of ribonuclease allows the proteins to be fused in-frame with ligand binding moieties to form cytotoxic fusion proteins. They can be used for treatment of cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rana pipiens ribonuclease Clone Salb; RaPLR1; covalently bound; RNase; LL2 antibody; ligand binding moiety; CD22; cancerous B cell; onconase; Kaposi's Sarcoma; human chorionic gonadotrophin; hCG; cancer; recombinant ribonuclease; frog; signal peptide; cytotoxic fusion protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MSDWLTFQKKHLTNTRDVDCNNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASK 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New recombinant ribonucleases, used for killing target cells, e.g. for treating cancers, viral infections or autoimmune diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MQNWATFQQKHIINT-PIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59 NVLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 105;
                                                                                                                                        'note= "Met not found in wild type RaPLR1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                           /note= "Wild type Gln replaced with Ser"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
46.4%; Score 281.5; DB 2;
Best Local Similarity 49.1%; Pred. No. 3e-24;
Matches 55; Conservative 15; Mismatches 33;
                                                                                                                                                                                                                                                                                                                                                     (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rana pipiens Clone 5alb ribonuclease.
                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY28879 standard; protein; 127 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 34; Page 61; 71pp; English.
                                                                                                                                                                                                                                                                                   99WO-US006641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                  autoimmune disease; RNase
                                                                                                                                                                                                                                                                                                                                                                                      Rybak SM, Newton DL;
                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1999-610847/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAZ08129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 105 AA;
                                                                                                                        Misc-difference
                                                                                                                                                         Misc-difference
                                                     pipiens.
                                                                                                                                                                                                                                                                                 26-MAR-1999;
                                                                                                                                                                                                                                                                                                                      27-MAR-1998;
                                                                                                                                                                                                                                                 07-CCT-1999,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-JAN-2000
                                                                      Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY28879;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 14
AAY28879
                                                     Капа
셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          à
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Ribonuclease; protein synthesis; inhibition; cancer; cytotoxic.

AAY39400 standard; protein; 105 AA.

(first entry)

01-DEC-1999

AAY39400;

Recombinant frog Onconase

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Recombinant Met(-1) Rana pipiens ribonuclease Met23Leu-(His)6; RaPLR1; CD22; covalently bound; LL2 antibody; ligand binding moiety; RNase; cancerous B cell; Kaposi's sarcoma; human chorionic gonadotrophin; hCG; signal peptide; recombinant ribonuclease; cytotoxic fusion protein; cancer; frog; autoimmune disease.
                                               Recombinant Met(-1) RaPLR1 Met23Leu-(His)6 protein.
                                                                                                                                                                                                                                                                          (USSH ) US DEPT HEALTH & HUMAN SERVICES.
standard; protein; 105 AA.
                                                                                                                                                                                                                                                                                                                                                          Claim 4; Page 59; 71pp; English.
                               (first entry)
                                                                                                                                                                                                                                                                                          Newton DL;
                                                                                                                                                                                                                                                                                                          WPI; 1999-610847/52.
N-PSDB; AAZ08127.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 105 AA;
                                                                                                                                                                                 Misc-difference
                                                                                                                                                Misc-difference
                                                                                                                                                                Misc-difference
                                                                                                                                                                                                                                         26-MAR-1999;
                                                                                                                 pipiens.
                                                                                                                                                                                                                                                         27-MAR-1998;
                                                                                                                                                                                                         WO9950398-A2
                                25-JAN-2000
                                                                                                                                                                                                                                                                                          Rybak SM,
                                                                                                                       Synthetic.
AAY28869
               AAY28869
                                                                                                                 Rana
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99WO-US006641 98US-0079751P

new recombinant Onconase used to treat, e.g. colon cancer.

Example 1; Fig 1; 42pp; English.

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Leung

Hansen H,

Goldenberg DM,

WPI; 1999-551416/46.

N-PSDB; AAZ19767

(IMMU-) IMMUNOMEDICS INC

'note= "(His)6 histidine tag attached to N-terminal Met"

/note= "Wild type Met replaced with Leu"

"Met not found in wild type RaPLR1"

'note=

Location/Qualifiers

99WO-US004252. 98US-0077557P.

11-MAR-1999; 11-MAR-1998;

WO9946389-A1

16-SEP-1999.

pipiens

Rana |

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concluded most of the N-certified of the C-ferminal and no acids of mature concoded most of the N-certified of the C-ferminal and the Conconse. The two PCR products generated encoded either the N-terminal 54 acids, and were ligated in frame that new or the C-terminal 51 amino acids, and were ligated in frame at an NruI site. The CDNA was then subcloned into a vector e.g., pBluescript, where the ATG initiation codon was ligated to the CDNA. After expression in B. coli, the recombinant protein was purified. The initial N-formyl methionine was cleaved off and pyroglutamate. The pyroglutamate residue cyclised to form an N-terminal pyroglutamate. The pyroglutamate residue forms part of the phosphate binding pocket of Onconaseand is essential for both ribonuclease and anti-tumour activity. Onconase is a 12 kD ribonuclease which causes cell death as a result of potent inhibition of protein synthesis by a mechanism involving inactivation of cellular RNA. It is not inhibited by mammalian placental ribonuclease inhibitor, which may explain its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          agents such as tamoxifen. When used as an anti-tumour agent, Onconase can
be conjugated to a marker which targets it to a specific cell type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  enhanced cytotoxicity relative to mammalian enzymes. It has anti-tumour activity against a variety of solid tumours e.g, colon or pancreatic cancers, and can be used alone or in combination with other anti-cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MQNWATFQQKHIINT-PIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence represents recombinant frog Onconase. Onconase has ribonuclease and anti-tumour activity. The cDNA was produced via PCR (using primers AAZ19768-Z19769) of two synthetic DNAs whose sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59 NVLSTTRFQLNTCTRISITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             46.5%; Score 282.5; DB 2 50.0%; Pred. No. 2.3e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50.0%; Pred. w.rive 15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            56; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 105 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence is a recombinant Rana piplens ribonuclease protein (RaPLRI) with Met at position 1 attached to (His)6 tag and Met24Leu. Carboxy terminal end of recombinant RaPLRI has a covalently bound ligand binding moiety, which can be a LL2 antibody directed against CD22 on cancerous B cells or human chorionic gonadotrophin (hCG) effective
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 against Kaposi's sarcoma cells. Recombinant ribonucleases can be expressed in bacteria without an N-terminal methionine due to the presence of a signal peptide that is cleaved by bacteria. The soluble expression of ribonuclease allows the proteins to be fused in-frame with ligand binding moieties to form cytotoxic fusion proteins. They can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New recombinant ribonucleases, used for killing target cells, e.g. for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MONWATFOOKHIINT-PIICNTIMDNNIYIVGGOCKRVNTFIISSATTVKAICTGVI-NM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59 NVLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          treating cancers, viral infections or autoimmune diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             used for treatment of cancer and autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  46.7%; Score 283.5; DB 2;
49.1%; Pred. No. 1.7e-24;
tive 16; Mismatches 32;
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4,

Gaps

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28 26

55; Conservative

Matches

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Best Local Similarity

Query Match

AAY28865 standard; protein; 104 AA.

AAY28865 ID AAY2

11 RESULT

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4.

Gaps

6

Indels

32;

Length 105;

DB 2;

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1 MONWATFQQKHIINT-PIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NM 58
                                                                                                                                         1 MODWLTFQKKHLTNTRDVDCNNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASK 56
                                                                                                                                                                              59 NVLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
                                                                                                                                                                                                  57 NVLTTSEFYLSDC---NVTSRPCKYKLKKSINTFCVTCENQAPVHFVGVGHC 105
                    47.2%; Score 286.5; DB: 50.0%; Pred. No. 7.9e-25. ive 15; Mismatches 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                     Antitumour protein from Rana pipiens oocytes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tumour; chemotherapy; radiotherapy; frog.
                                                                                                                                                                                                                                                                                                                   AAW06544 standard; protein; 104 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 8; Page 28; 45pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95US-00467955.
                  Query Match
Best Local Similarity 50.0%
Matches 56; Conservative
                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            55; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (ALFA-) ALFACELL CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1997-043063/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 104 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pipiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9639428-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    03-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                              22-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ardelt WJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is a recombinant Rana pipiens ribonuclease (RaPLRI) protein with Met at position 1. Carboxy terminal end of recombinant RaPLRI has a covalently bound ligand binding moiety, which can be a LLZ antibody directed against CD22 on cancerous B cells or human chorionic gonadorrophin (hCG) effective against Kaposi,'s sarcoma cells. Recombinant ribonucleases can be expressed in bacteria without an N-terminal methionine due to the presence of a signal peptide that is cleaved by bacteria. The soluble expression of ribonuclease allows the proteins to be fused in-frame with ligand binding moieties to form cytotoxic fusion proteins. They can be used for treatment of cancer and autoimmune
                                                                                                                                                                                Recombinant Met(-1) Rana pipiens ribonuclease; RaPLR1; CD22; RNase; coalentuly bound; LL2 antibody; ligand binding moiety; cancerous B cell; Kaposi's sarcoma; human chorionic gonadotrophin; hCG; signal peptide; recombinant ribonuclease; cytotoxic fusion protein; cancer; frog;
                                                                                                                                                         2 QNWATFQQKHIINTFII-CNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNV 60
(Rana catesbeiana) lectin used to describe the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              for
                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New recombinant ribonucleases, used for killing target cells, e.g. treating cancers, viral infections or autoimmune diseases.
                                                                                                                                                                                                                                     61 LSTTRFQLNTCTRTSITPRPCPYSSRTEINYICVKCENQYPVHFAGIGRCP 111
                                                                                                                                                                                                                                                           61 LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
                                                                                                                    1;
                                                                               Length 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "Met not found in wild type RaPLR1"
                                                                                                                    Indels
                                                                             Score 588.5; DB 2;
Pred. No. 2.2e-59;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                          AAY28867 standard; protein; 105 AA.
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                                                                             97.0%;
98.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Recombinant Met(-1) RaPLR1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                Matches 109, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               autoimmune disease.
                                                                                                Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAZ08126.
                                      Sequence 111 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rana pipiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-CCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                               AAY28867;
                                                                             Query Match
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AAY28867 RESULT

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                                                                                                                                                                           The present sequence is a specifically claimed example of an antitumour protein from the generic protein in AAW18224, with the molecular weight 12000. This is one of two preferred proteins (the other in AAW6543) that have been isolated from Rana pipiens occytes. Both proteins have a blocked amino terminal group and are essentially free of carbohydrates. The proteins are used to treat tumours. Use of the peptides has fewer disadvantages than chemotherapy, radiotherapy and surgery in the treatment of tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 QNWATFQQKHIINT-PIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NMN 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60 VLSTTRFQLNTCTRTSITPRPCPYSSRIETNYICVKCENQYPVHFAGIGRC 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57 VLTISEFYLSDC---NVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGRC 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 104;
Antitumour proteins from Rana pipiens oocyte(s) - have fewer disadvantages than chemotherapy, surgery and radiotherapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  46.9%; Score 284.5; DB 2;
49.5%; Pred. No. 1.3e-24;
live 16; Mismatches 31;
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RESULT 10 AAY28869

Sequence 105 AA;

diseases

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The present sequence is a recombinant Rana catesbeiana oocyte ribonuclease (RaCOR1) protein with Met22Leu Met57Leu. Carboxy terminal end of recombinant RaCOR1 has a covalently bound ligand binding molety, which can be a LLZ antibody directed against CD22 on cancerous B cells or human chorionic gonadotrophin (hCG) effective against Kaposi's sarcoma cells. Recombinant ribonucleases can be expressed in bacteria without an N-terminal methionine due to the presence of a signal peptide that is cleaved by bacteria. The soluble expression of ribonuclease allows the proteins to be fused in-frame with ligand binding moleties to form cytotoxic fusion proteins. They can be used for treatment of cancer and
                                                                                                               3 NWAIFQQKHIINTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNVLS 62
                                                                                                                                                                                                                                                                                                                                                                                                     Recombinant Rana catesbeiana oocyte ribonuclease; covalently bound; RaCORI Met22Leu, LL2 antibody; ligand binding moiety; CD22; cancerous B cell; Kaposi's sarcoma, human chorionic gonadotrophin; hCG; signal peptide; recombinant ribonuclease; cytotoxic fusion protein;
                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New recombinant ribonucleases, used for killing target cells, e.g. treating cancers, viral infections or autoimmune diseases.
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                                                                                                                                                           TTRFQLNTCTRTSITPRPCPYSSRTEINYICVKCENQYPVHFAGIGRCP 111
                            Length 110;
                                                                                                                                                                              TTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP
                                                                                                                                                                                                                                                                                                                                                                      Recombinant RaCOR1 Met22Leu Met57Leu amino acid sequence.
                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "Wild type Met replaced with Leu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "Wild type Met replaced with Leu"
                                                              .;
0
                            Score 597; DB 2; I
Pred. No. 2.3e-60;
                  98.4%; Scc...
100.0%; Pred. No. ...
... 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cancer; bullfrog; RNase; autoimmune disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (USSH ) US DEPT HEALTH & HUMAN SERVICES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                         AAY28874 standard; protein; 110 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 22; Page 64; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99WO-US006641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98US-0079751P
                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rybak SM, Newton DL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1999-610847/52.
N-PSDB; AAZ08132.
                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rana catesbeiana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Misc-difference
Sequence 110 AA,
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                                                            Matches 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic
                                                                                                                                                                                                                                                                                                         AAY28874;
                                                                                                                                                             63
                              Query Match
Best Local
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autoimmune diseases

Sequence 110 AA;

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This invention describes a novel nucleic acid construct comprising sequences encoding functional pancreatic RNase and a second protein (preferably the light and heavy chains of an antibody) which binds a specific cell surface marker on a target cell and functions as a cytotoxic agent. The products can be used for selectively killing cells cytotoxic agent. The products can be used for treating tumors or infected cells (e.g. cells infected by viruses (especially latent or chronic virus infections, such as human immunodeficiency virus latent or chronic virus infections, such as human immunodeficiency virus (HIV)-1, Epstein-Barr virus, herpes viruses (herpes simplex types I and II), hepatitis viruses (B, non-A-non-B, and delta), herpes toster, cytomegalovirus) and cells infected with parasites (such as the malaria parasite)). They can also be used for treating immune dysfunctional cells in immune and autoimmune diseases. Additionally, they may be used as contraceptives. Finally they can also be used for cell separation in vitro by selectively killing unwanted types of cells (e.g. in bone marrow) prior to transplantation into a patient undergoing marrow ablation by radiation or for killing leukemia cells or T-cells that would cause graft-versus-host disease. This sequence represents a bullfrog
                                       0;
                                                                              QNWATFQQKHIINTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNVL 61
                                                                                                     1 QNWATFQQKHIINTPIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINLNVL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cytotoxic; RNase, ribonuclease; pancreatic; antibody; light chain; heavy chain; cell surface marker; treatment; tumor; viral infection; parasite infection; immune dysfunctional cell; autoimmune disease; contraceptive; cell separation; transplantation; bone marrow ablation; leukemia cell; T-cell; graft-versus-host disease; bullfrog; lectin.
                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Recombinantly fused pancreatic RNase-targeting proteins useful for treating tumors, infections, immune or autoimmune disorders and as
                                                                                                                                                             62 STTRFQLNTCTRISITPRPCPYSSRIETNYICVKCENQYPVHFAGIGRCP 111
                                                                                                                                                                                 ;
0
                                       0; Indels
DB 2;
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Score 596; DB 2;
Pred. No. 3e-60;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 3; Fig 19; 47pp; English.
                                                                                                                                                                                                                                                                                                 AAY33321 standard; protein; 111
                                                                                                                                                                                                                                                                                                                                                                                                                       lectin protein fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        90US-00510696.
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    98.2%;
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                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rybak SM, Newton DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1999-560488/47.
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rana catesbeiana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-SEP-1993;
                                                                                                                                                                                                                                                                                                                                                                                 29-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-APR-1990;
22-OCT-1991;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JS5955073-A.
                                         108;
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                                                                                                                                                                                                                                                                                                                                                                                                                         Frog
                                         Matches
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Gaps

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Query Match Best Local

Matches

61

RESULT 4 AAY28876

61

AAY28876;

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covalently bound; LL2 antibody; ligand binding moiety; cancerous B cell; bullfrog; Kaposl's sarcoma; human chorionic gonadotrophin; hCG; RNase; signal peptide; recombinant ribonuclease; cytotoxic fusion protein; cancer; autoimmune disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Recombinant Rana catesbeiana oocyte ribonuclease; RaCOR1 Gln1Ser; CD22;
                                                                                                                                                                                                                              1 MONWATFQOKHIINTPIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINLNV
                                                                                                                                                                                         1 MONWATFOOKHIINTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNV
  proteins. They can be used for treatment of cancer and autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New recombinant ribonucleases, used for killing target cells, treating cancers, viral infections or autoimmune diseases.
                                                                                                                                                                                                                                                                                                  LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP
                                                                                                                                                                                                                                                                          61 LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP
                                                                                                           Length 111;
                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "Wild type Gln replaced with Ser"
                                                                                                                                                  0
                                                                                                        Score 601; DB 2;
Pred. No. 8.1e-61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Recombinant RaCOR1 Gln1Ser amino acid sequence.
                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                      AAY28877 standard; protein; 110 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 22; Page 67; 71pp; English.
                                                                                                                                                2;
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                                                                                                        99.0%;
98.2%;
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                                                                                                                                                109; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Newton DL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1999-610847/52.
                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rana catesbeiana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Key
Misc~difference
                                                               Sequence 111 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAZ08134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-JAN-2000
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                                                                                                      Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY28877;
                   diseases
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Matches
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                                                                                                                                                                                                                                                                                                                                                                               RESULT 5
ឧដ្ឋទ
                                                                                                                                                                                                                              a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Met(-1) Rana catesbeiana ribonuclease Met22Leu Met57Leu-(His)6; RaCOR1; recombinant; CD22; covalently bound; LLZ antibody; ligand binding moiety; cancerous B cell; Kaposi's sarcoma; human chorionic gonadotrophin; hCG; signal peptide; recombinant ribonuclease; cytotoxic fusion protein; cancer; bullfrog; RNase; autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence is a recombinant Rana catesbelana occyte ribonuclease (RaCOR1) protein with Met at position 1 attached to a (His)6 tag, Met23Leu and Met68Leu. Carboxy terminal end of recombinant RaCOR1 has a covalently bound ligand binding moiety, which can be a LL2 antibody directed against CD22 on cancerous B cells or human chorionic gonadotrophin (hCG) effective against Kaposi's sarcoma cells. Recombinant ribonucleases can be expressed in bacteria without an N-terminal methionine due to the presence of a signal peptide that is cleaved by bacteria. The soluble expression of ribonuclease allows the proteins to be fused in-frame with ligand binding moieties to form cytotoxic fusion
                                                                                                    9
                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note= "(His)6 histidine tag attached to N-terminal Met"
                                                                                                                              MSNWATFQQKHIINTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINNVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             for
                                                                                                MQNWATFQQKHIINTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNV
                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   recombinant ribonucleases, used for killing target cells, e.g.
                                                                                                                                                                                LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
                                                                                                                                                                                                                              111
                                                          ٠,
                                                                                                                                                                                                        LSTTRFQLNTCTRTSITPRFCPYSSRTETNYICVKCENQYPVHFAGIGRCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Recombinant Met(-1) RaCOR1 Met22Leu Met57Leu-(His)6 protein.
               Length 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note= "Met not found in wild type RaCOR1"
                                                        1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note= "Wild type Met replaced with Leu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "Wild type Met replaced with Leu"
             Score 602; DB 2;
Pred. No. 6.2e-61;
0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                              AAY28876 standard; protein; 111 AA.
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             99.2%;
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                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rybak SM, Newton DL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1999-610847/52.
                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             catesbeiana.
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                                                                                                                                                                                                                                                                                                                                                                                                             25-JAN-2000
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                                                  110;
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Rana cates Synthetic.

human

for

e.g.

treating

CCCCCCCCCXXXXXIBXXBXXBXXBXXBXBXBIIIIIIXX8XXXXXXXBXBX

0

Gaps

., 0

Indels

99.2%; Score 602; DB 2; 100.0%; Pred. No. 6.1e-61; ive 0; Mismatches 0;

Matches 110; Conservative

Query Match Best Local Similarity

Sequence 110 AA;

80

Length 110;

61 9

1 QNWATFQQKHIINTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNVL 2 QNWATFQQKHIINTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNVL

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61 STTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110

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AAY28878 standard; protein; 111

RESULT 3

62 STIRFQLNICIRISIIPRPCPYSSRIEINYICVKCENQYPVHFAGIGRCP

111

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0;
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                                                                                                                                                                                                                                                                                                                                                                                                                  Rana catesbeiana oocyte ribonuclease; RaCOR1; covalently bound; CD22; LL2 antibody; Ligand binding moiety; camcerous B cell; Raposi's Sarcoma; human chorionic gonadotrophin; PGC; recombinant ribonuclease; bullfrog; signal peptide; cytotoxic fusion protein; cancer; autoimmune disease;
Recombinant ribonucleases can be expressed in bacteria without an
          N-terminal methionine due to the presence of a signal peptide that is cleaved by bacteria. The soluble expression of ribonuclease allows the proteins to be fused in-frame with ligan binding moleties to form cytotoxic fusion proteins. They can be used for treatment of cancer and
                                                                                                                                                                  1 MQNWATFQQKHIINTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNV
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                                                                                                                                         0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                          Rana catesbeiana oocyte ribonuclease (RaCOR1) amino acid sequence.
                                                                                                                                                                                                                      61 LSTTRFQLNTCTRISITPRPCPYSSRTEINYICVKCENQYPVHFAGIGRCP 111
                                                                                                                                                                                                                                  LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP
                                                                                                                Length 111;
                                                                                                                                         Indels
                                                                                                                Score 607; DB 2;
Pred. No. 1.7e-61;
                                                                                                                                           Mismatches
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                                                                                                                                                                                                                                                                                                             AAY28872 standard; protein; 110
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                                                                                                                 100.0%;
100.0%;
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                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                           Conservative
                                                                autoimmune diseases
                                                                                                                Query Match
Best Local Similarity
Matches 111; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rana catesbeiana
                                                                                        Sequence 111 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic
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The present sequence is a recombinant Rana catesbelana ribonuclease (RaCORI) protein with Met at position 1 and Gln2Ser. Carboxy terminal end of recombinant RaCORI has a covalently bound ligand binding moiety, which can be a LL2 antibody directed against CD22 on cancerous B cells or human chorionic gonadotrophin (hCG) effective against Kaposi's sarcoma cells. Recombinant ribonucleases can be expressed in bacteria without an N-terminal methionine due to the presence of a signal peptide that is cleaved by bacteria. The soluble expression of ribonuclease allows the proteins to be fused in-frame with ligand binding moieties to form cytotoxic fusion proteins. They can be used for treatment of cancer and
                                                                                                          Recombinant Met(-1) Rana catesbeiana oocyte ribonuclease GlnlSer; RaCOR1; covalently bound; LL2 antibody; ligand binding moiety; cancerous B cell; Kaposi's sarcoma, human chorionic gonadotrophin; hCG; signal peptide; recombinant ribonuclease; cytotoxic fusion protein; cancer; bullfrog; CD22; RNase; autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New recombinant ribonucleases, used for killing target cells, e.g. for treating cancers, viral infections or autoimmune diseases.
                                                                                                                                                                                                                                                                                                       not found in wild type RaCOR1"
                                                                                                                                                                                                                                                                                                                                       /note= "Wild type Gln replaced with Ser"
                                                                               Recombinant Met(-1) RaCOR1 Gln1Ser amino acid sequence.
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                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 22; Page 68; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                          99WO-US006641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98US-0079751P
                                                                                                                                                                                                                                                                                                       'note= "Met
                                                 (first entry)
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                                                                                                                                                                                                                      Rana catesbeiana
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                                                                                                                                                                                                                                                                                       Misc-difference
                                                                                                                                                                                                                                                                                                                         Misc-difference
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                                                 25-JAN-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rybak SM,
                                                                                                                                                                                                                                       Synthetic.
                 AAY28878;
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Sequence 111 AA;

The present sequence is a Rana catesbeiana oocyte ribonuclease (RacOR1) protein encoded by a cDNA modified for expression in E. coli. Carboxy terminal end of RaCOR1 has a covalently bound ligand binding moiety, which can be a LL2 antibody directed against CD22 on cancerous B cells or human chorionic gonadotrophin (hCG) effective against Kaposi's Sarcoma cells. Recombinant ribonucleases can be expressed in bacteria without an A-terminal methionine due to the presence of a signal peptide that is cleaved by bacteria. The soluble expression of ribonuclease allows the proteins to be fused in-frame with ligand binding moieties to form

autoimmune diseases

for

cells, e.g.

New recombinant ribonucleases, used for killing target cel treating cancers, viral infections or autoimmune diseases.

Rybak SM, Newton DL; WPI; 1999-610847/52. N-PSDB; AAZ08130. Claim 22; Page 62; 71pp; English.

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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
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7, 2004, 21:25:55 ; Search time 47.3489 Seconds (without alignments) 662.376 Million cell updates/sec May Run on:

US-09-961-400-17

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1 MONWATFQOKHIINTPIICN.....iCVKCENQYPVHFAGIGRCP Sequence:

111

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1586107 segs, 282547505 residues Searched:

1586107 Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000 sed BB BB Minimum I Maximum I

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

.. Database

A_Geneseq_29Jan04:* L: geneseqp1980s:* 2: geneseqp1990s:* geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* geneseqp2000s:* geneseqp2001s:* geneseqp2004s:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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277.5						272.5		272.5		•	į.	268.5

ALIGNMENTS

RESULT 1

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Recombinant Met (-1) Rana catesbeiana oocyte ribonuclease; RaCOR1; CD22; covalently bound; LL2 antibody; ligand binding moiety; cancerous B cell; Kaposi's sarcoma; human chorionic gonadotrophin; hCG; signal peptide; recombinant ribonuclease; cytotoxic fusion protein; cancer; bullfrog; RNase; autoimmune disease.
                                                                                                                                                                     /note= "Met not found in wild type RaCOR1"
                                                                                                                                                    Location/Qualifiers
AAY28873 standard; protein; 111 AA.
                                                                                                                                                                                                                         99WO-US006641.
                                                    Recombinant Met(-1) RaCOR1.
                                   (first entry)
                                                                                                                         Rana catesbeiana.
                                                                                                                                                           Misc-difference
                                                                                                                                                                                      WO9950398-A2
                                                                                                                                                                                                                         26-MAR-1999;
                                   25-JAN-2000
                                                                                                                                                                                                       07-OCT-1999.
                                                                                                                                    Synthetic.
                  AAY28873;
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(USSH) US DEPT HEALTH & HUMAN SERVICES. 98US-0079751P. Newton DL; WPI; 1999-610847/52. N-PSDB; AAZ08131 27-MAR-1998; Rybak SM,

New recombinant ribonucleases, used for killing target cells, e.g. for treating cancers, viral infections or autoimmune diseases.

Claim 22; Page 63; 71pp; English.

or The present sequence is a recombinant Rana catesbeiana oocyte ribonuclease (RaCOR1) protein with Met at position 1. Carboxy terminal end of recombinant RaCOR1 has a covalently bound ligand binding moiety, which can be a LL2 antibody directed against CD22 on cancerous B cells human chorionic gonadotrophin (hCG) effective against Kaposi's sarcoma

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                                                                                                                                                                                                                    Beintema J.J.; Recretory ribonuclease genes and pseudogenes in true ruminants."; "Secretory ribonuclease genes and pseudogenes in true ruminants."; ene 212:259-268(1998).
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 21.2%; Score 127.5; DB 1; Length 151; Best Local Similarity 30.6%; Pred. No. 8.7e-07; Matches 37; Conservative 17; Mismatches 44; Indels 23;
                                                                                                                                                                                             EMBL; Y11670; CAA72368.1; -. HSSP; P00656; 1SRN.
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SEQUENCE OF 31-114 FROM N.A.
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Giraffoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13; Gaps
                                                                                                                                                                                                        -- purification and
                                                                                                                                                      Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21.2%; Score 127.5; DB 1; Length 123; 30.6%; Pred. No. 7e-07; Live 19; Mismatches 43; Indels 13.
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14522 MW; B703B9839919FD2F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Prodom, PD000535; RNaseA; 1.
SMART; SM00092; RNASe Pc; 1.
PROSITE; PS00127; RNASE PANCERATIC; 1
Hydrolase; Nuclease; Endonuclease; Androgenesis;
Protein synthesis inhibitor; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q29542; Q29533;
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Ribonuclease, brain (EC 3.1.27.-) (BRB).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00074; rnaseA; 1.
PRINTS; PR00794; RIBONUCLEASE.
ProDom; PD000535; RNaseA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001427; RNaseA.
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39
113
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          Mammalia; Eutheria; Ce
Bovidae; Bovinae; Bos
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                                          Bovidae; Bovinae
NCBI_TaxID=9913;
                                                                                                                                           TISSUE=Milk,
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RNBR GIRCA
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            Breukelman H.J., Beintema J.J., Confalone E., Costanzo C., Sasso M.P., Carsana A., Palmieri M., Furia A., "Sequences related to the ox pancreatic ribonuclease coding region in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidea;
Cervidae; Cervinae; Axis.
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N-LINKED (GLCNAC. . .) (BY SIMILARITY).

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Breukelman H.J., van der Munnik N., Kleineidam R.G., Furia A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21.2%; Score 127.5; DB 1; Length 141; 30.6%; Pred. No. 8.1e-07;
                                                                                                                                              J. Mol. Evol. 37:29-35(1993).
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ProDom, PD000535, American 1.

SMART; SM00092; RNASE PANCEATIC; 1.

PROSITE; PS00127; RNASE PANCEATIC; 1.

Hydrolase; Nuclease; Endonuclease; Glycoprotein.

41

PY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AXIPR
RNBR AXIPR
RNBR AXIPR
P87350;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 41, Last annotation update)
15-DEC-1998 (Rel. 41, Last annotation update)
15-DEC-1998 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17; Mismatches
                                                                                                                the genomic DNA of mammalian species.";
MEDLINE=93367815; PubMed=8360916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41 BY
84 BX
84 BX
110 BY
72 BY
62 N-
129 N-
1592 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00074; rnaseA; 1.
PRINTS; PR00794; RIBONUCLEASE.
ProDom; PD000535; RNaseA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; S81743; AAB36137.1; -. EMBL; S65126; AAB27931.1; -. HSSP; P00656; 2RNS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001427; RNaseA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          58 NVL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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CAPCA
                                                                                                                                                                Beintema J
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P80929;
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                                                        6 FQQXHI-----INTPLICUTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGV-INMN 58
                                                                                 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59
                                                                     1 QNWATFQQKHI-----INTPILCNTIMDNNIYIVGGQCKRVNTFIISSATTVKAIC--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ODWSSFONKHIDYPETSASNPNAYCDLMMORR-NLNPTKCKTRNTFVHASPSEIQQVCGS
                                                                                             59 VLSTTRFQLNT-----CTRISITPRP-CPYSSRTEINYICVKCENQ--YPVHF 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    52 --IGVINMAVLSTTRFQLNTCTRISIT-PRPCPYSSRTETNYICVKCENQYPVHF 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGTHYEDNLYDSNESFDLTDCKNVGGTAPSSCKYNGTPGTKRIRIACENNQPVHF 114
                                                                                                                                                                                                                                                                                                                                               3'-
U-P
                                                                                                                                                                                                                                                                                                                                                                                                                                         R Prodom; PD000535; RNASE PC; 1.

R PROSITE; PS00127; RNASE PC; 1.

R PRACOLAGE; RNASE PC; 1.

R Hydrolase; Nuclease; Endonuclease; Pyrrolidone carboxylic acid.

FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.

FT DISULRID 25 80 BY SIMILARITY.

FT DISULRID 39 91 BY SIMILARITY.

FT DISULRID 57 106 BY SIMILARITY.

FT ACT SITE 10 10 BY SIMILARITY.

FT ACT SITE 10 10 BY SIMILARITY.

FT ACT SITE 13 113 BY SIMILARITY.

FT ACT SITE 13 13324 MW; 6072FB5B7B15BD5A CRC64;
                                                                                                                                                                                                                                Būkaryotā; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
                                                                                                          17;
                                                                                                                                                                                                                                                                                                                            13;
                     Score 132.5; DB 1; Length 124;
Pred. No. 2e-07;
9; Mismatches 42; Indels 17,
                                                                                                                                                                                                                                         Lepidosauria, Squamata, Iguania, Iguanidae, Iguaninae, Iguana
NCBI_TaxID=8517,
                                                                                                                                                                                                                                                                                                  Zhao W., Beintema J.J., Hofsteenge J.;
"The amino acid sequence of iguana (Iguana iguana) pancreatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 119;
                                                                                                                                                                                 01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Ribonuclease pancreatic (EC 3.1.27.5) (RNase A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51; Indels
   OAC28CDE14111845 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21.8%; Score 131.5; DB 1
30.4%; Pred. No. 2.5e-07;
ive 16; Mismatches 51
                                                                                                                                                                   119 AA.
                 22.0%; Scor
31.6%; Pred
                                                                                                                                                                                                                                                                                        MEDLINE=94139745; PubMed=8307028;
  13804 MW;
                                                                                                                                                                                                                       Iguana iguana (Common iguana).
                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam, PF00074, rnaseA; 1.
PRINTS, PR00794, RIBONUCLEASE.
ProDom; PD000535; RNaseA; 1.
                                                                                                                                                                                                                                                                                                                                                                                              PIR; S41111; S41111.
HSSP; P00656; 1LSQ.
InterPro; IPR001427; RNaseA.
                                       36; Conservative
                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
  124 AA;
                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                TISSUE=Pancreas;
                                                                                                                                                                                                                                                                                                                      ribonuclease.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35;
                                                                                                                                                                RNP IGUIG
P80287;
SEQUENCE
                                                                                                                                                                                                                                                                       SEQUENCE
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                                       Matches
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RESULT 12

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ## BEBL: Y11673; C.

## BMBL: Y11673; C.

## BMBL: PR0040427; RNa.

## PF00074; rnaseA; 1.

## PR00074; RNaseA; 1.

## PR00072; RNaseA; 1.

## PR011E; P800127; RNASE PANCREATIC; 1.

## PR012E; P800127; RNASE PANCREATIC; 1.

## PR012E; P800127; RNASE PANCREATIC; 1.

## PR012E; P80012T; RNASE PANCREATIC; P80012E; P8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 ATFQQKHI-----INTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINM 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AKFRRQHMDSGSSSGNPNYCNQMMKRR-RMTHGRCKPVNTFVHESLDNVKAVCS---QK 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NVL------STTRFQLNTCTRTSITPRP-CPYSSRTETNYICVKCENQ--YPVHF 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62 NITCKNGQPNCYQSNSTWNITDCRQTGSSKYPNCAYKTSQKQKYİTVACBGDPYVPVHF 120
                                                                    15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
Ribonuclease, brain (EC 3.1.27..) (BRB).
Capreolus capreolus (Roe deer).
Eukaryota, Metazoa; Chordata, Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Cetarriodactyla; Ruminantia; Pecora; Cervoidea;
Cervidae; Odocoileinae; Capreolus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Secretory ribonuclease genes and pseudogenes in true ruminants.";
Gene 212:259-268(1998).
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Breukelman H.J., van der Munnik N., Kleineidam R.G., Furia A.,
    151 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-REP-2003 (Rel. 41, Last annotation update)
Angiogenin-2 (EC 3.1.27.-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    123 AA
    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=98278842; Pubmed=9611269;
STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9858;
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ID ANG2_BC
ANG2_BC
DT 01-NOV.
DT 28-FEB-
DE ANG1000
GN ANG2.
CS BOSTON
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124 AA
17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=70104198; PubMed=4904878;
                                                                                                                                                                                                                                                                                                                                        MEDLINE=70104197; PubMed=5460946;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS, PR00794; RIBONUCLEASE. ProDom; PD000535; RNaseA; 1. SMART; SM0092; RNAse_Pc; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR; A92071; NRPG.
HSSP; P00656; 1SRN.
InterPro; IPR001427; RNaseA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00074; rnaseA; 1
 38; Conservative
                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 884
110
172
113
119
76
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                                                                                                                                                                                                                                                                                                                                                                                                           REVISION TO 2.
                                                                                                               105 G 105
                                                                                                                                                                                                                                                            RNASE1 OR RNS1
                                                                                                                                   148 G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACT_SITE
ACT_SITE
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CARBOHYD
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                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                          RNP PIG
                                                                                                                                                                     RESULT 10
  Matches
                                                                                                                                                                                 RNP_PIG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                             MEDILINE=92093604; PubMed=1754384; Sasso M.P., Carsana A., Confalone E., Cosi C., Sorrentino S., Viola M., Palmieri M., Russo E., Furia A.; "Molecular cloning of the gene encoding the bovine brain ribonuclease and its expression in different regions of the brain."; Nucleic Acids Res. 19:6469-6474(1991).
                                   Bos taurus (Bovine).
Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinee; Bos.
                                                                                                                                                                                                                           Watanabe H., Katoh H., Ishii M., Komoda Y., Sanda A., Takizawa Y., Ohgi K., Irie M.,
"Primary structure of a ribonuclease from bovine brain.";
                                                                                                                                                                                                                                                                                            MEDLINE=96139017; PubMed=8587129;
Confalone B., Beintema J.J., Sasso M.P., Carsana A., Palmieri M.,
Vento M.T., Furia A.;
"Molecular evolution of genes encoding ribonucleases in ruminant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 133.5; DB 1; Length 167; Pred. No. 2.2e-07;
                                                                                                                                                                                                                                                                                                                                                      J. Mol. Evol. 41:850-858(1995).
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ProDom; PD000535; RNaseA; 1.
SMART; SM00092; RNASe Pc; 1.
PROSITE; PS00127; RNASE PANCREATIC; 1.
Hydrolase; Nuclease; Endonuclease; Glycoprotein; Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -> S (IN REF. 2).
681CAAC3CC2FC459 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
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BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. ..).
/FIId=CAR_000005.
                                                                                                                                                                                             SEQUENCE OF 27-167, AND CARBOHYDRATE-LINKAGE SITES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RIBONUCLEASE, BRAIN
    16-OCT-2001 (Rel. 40, Last annotation update)
Ribonuclease, brain precursor (EC 3.1.27.-) (BRB)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       O-LINKED.
O-LINKED.
                                                                                                                                                                                                                     MEDLINE=89214015; PubMed=3243767;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP, P00656; 2RNS.
GlycoSuiteDB; P39873; -.
InterPro; IPR001427; RNaseA.
Pfam; PF00074; rnaseA, 1.
PRINTS; PR00794; RIBONUCLEASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       155 O.
159 O.
155 T
                                                                                                                                                                                                                                                                Biochem. 104:939-945(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22.2%;
31.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X59767; CAA42439.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; S81744; AAB36138.1; -. S20066; S20066.
                                                                                                                                                                                                                                                                            [3] SEQUENCE OF 27-167 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              155
167 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
                                                                                                         SEQUENCE FROM N.A.
                                                                                 NCBI_TaxID=9913;
                                                                                                                                                                                                           TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACT_SITE
ACT_SITE
ACT_SITE
DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CARBOHYD
                                                                                                                                                                                                                                                                                                                                                species.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHAIN
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58 NVL-----STTRFQLNTCTRTSITPRP-CPYSSRTETNYICVKCE-NQY-PVHFA 104
                                                                                                                                                                                                                                                       88 NITCRNGHPNCYQSKSIMSIIDCREIGSSKYPNCAYKISQKQKYIIVACEGNPYVPVHFD 147
                                                              4 ATFQQKHI------INTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINM 57
                                                                                                                             32 AKFRROHMDSGSSSSSNPNYCNOMMKRR-RMTHGRCKPVNTFVHESLDDVKAVCS---QK 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wierenga R.K., Huizinga J.D., Gaastra W., Welling G.W., Beintema J.J.; "Affinity chromatography of porcine pancreatic ribonuclease and reinvestigation of the N-terminal amino acid sequence."; FEBS Lett. 31:181-185(1973).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    phelan J.J., Hirs C.H.W.;

"The primary structure of porcine pancreatic ribonuclease. 3. The disulfide bonds."

J. Blol. Chem. 245:654-661(1970).

-!- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'--
phosphates and 3'-phospholigonucleotides ending in C-P or U-P
with 2', 3'-cyclic phosphate intermediates.

-!- SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Jackson R.L., Hirs C.H.W.;
"The primary structure of porcine pancreatic ribonuclease. II.
amino acid sequence of the reduced S-aminoethylated protein.";
J. Biol. Chem. 245:637-653 (1970).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- TISSUE SPECIFICITY: Pancreas.
-!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
28-FEB-2003 (Rel. 41, Last amoncation update)
Ribonuclease pancreatic (EC 3.1.27.5) (RNase A)
43; Indels
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N-LINKED (GLCNAC. ..).
N-LINKED (GLCNAC. ..).
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Hydrolase; Nuclease; Endonuclease; Glycoprotein.
DISULFID 26 я4
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137
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DISULFID
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RE STEAIN=FVB/N; TISSUE=Liver;

RA STRAIN=FVB/N; TISSUE=Liver;

RA STRAIN=FVB/N; TISSUE=Liver;

RA Alsaberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Alsachul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Raha S.A., WcEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Rahards S. Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Rahay J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

RA Miting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Rodriguez A.C., Grimwood J., Schwutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                      6 FQQKHII-----NTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNV 59
                                                                                                                                                                                                                                                     L-----STTRFQLNTCTRISITPRP-CPYSSRTETNYICVKCE-NQY-PVHF 103
                                                                                                                                                                                                                                                                                            64 LCKNGRINCYESNSTWHITDCRQIGSSKYPNCAYKTSQKEKHIIVACEGNPYVPVHF 120
                                                                                                                                                                                                                      23; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                  01-MAY-1991 (Rel. 18, Created)
01-MAY-1991 (Rel. 18, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Angiogenin precursox (EC 3.1.27.-) (Ribonuclease 5) (RNase 5).
                                                                                                                                                                                                Score 135.5; DB 1; Length 124; Pred. No. 9.7e-08;
                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=91025023; PubMed=2222458;
Bond M.D., Vallee B.L.;
"Isolation and sequencing of mouse angiogenin DNA.";
Biochem. Biophys. Res. Commun. 171:988-995(1990).
                                                                                                                                                                                                                      39;
                                                                                                                                                                                                           ; Pred. No. 9.7e-
16; Mismatches
                                                                                                                                                                                                                                                                                                                                                        145 AA.
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PIR; A00818; NRWHK.
HSSP; P00656; LSRN.
InterPro; IPRO1427; RNaseA.
Pfam; PF00074; rnaseA; 1.
PRINTS; PR00794; RIBONUCLEASE.
ProDom; PD000535; RNaseA; 1.
                                                                                                                                                                                                 22.5%;
                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse)
                                                                                                                                                                                                         Similarity
39; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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                                                                                                                                                                                                                                                   Biochim. Biophys. Acta 1162:177-186(1993).

-I-FUNCTION: May function as a tRNA-specific ribonuclease that binds to actin on the surface of endothelial cells; once bound, angiogenin is endocytosed and translocated to the nucleus, thereby promoting the endothelial invasiveness necessary for blood vessel formation. Angiogenin induces vascularization of normal and malignant tissues. Abolishes protein synthesis by specifically hydrolyzing cellular tRNAs.

-SUBCELLULAR LOCATION: Secreted.

SIMILARITY: Belongs to the pancreatic ribonuclease family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00074; rnaseA; 1.
PRINTS; PR00794; RIBONUCLEASE.
PRINTS; PR00794; RIBONUCLEASE.
SMART; SM00092; RNASE PC; 1.
PROSITE; PS00127; RNASE PANCREATIC; 1.
Hydrolase; Nuclease; Endonuclease; Angiogenesis;
Protein synthesis inhibitor; Signal; Pyrrolidone carboxylic acid.
                                                                                                       TISSUE=Serum;
MEDLINE=93192291; PubMed=8448182;
Bond M.D., Strydow D.J., Vallee B.L.;
"Characterization and sequencing of rabbit, pig and mouse angiogenins: discernment of functionally important residues and regions.";
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human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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(Rel. 31, Last sequence update)
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Pred. No. 1.16
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EMBL, BCO55355, AAH55355.1; -.
PIR, A35932, A3593.
HSSP, P03950, 1A4Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        88 TNYICVKCENQYPVHF 103
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39.5%;
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InterPro; IPR001427; RNaseA.
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RNBR_BOVIN
ID RNBR_BOVIN
AC P39873;
DT 01-FEB-1995 (
DT 01-FEB-1995 (
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43.48;
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                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33 CKRVNTFIISSATTVKAIC-----TGVINMNVLSTTRFQLNTCTRISITPR-PCPYSSR 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=129; TISSUE=Liver;
MEDLINE=96079109; PubMed=8530072;
Brown W.E., Nobile V., Subramanian V., Shapiro R.;
"The mouse anglogenin gene family: structures of an anglogenin-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                    FUNCTION: Anglogenin induces vascularization of normal and malignant tissues. Abolishes protein synthesis by specifically hydrolyzing cellular tRNAs (By similarity). SIMILARITY: Belongs to the pancreatic ribonuclease family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata, Craniata, Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00127; RNAGE PANCREATIC; 1.
Hydrolase; Nuclease; Endonuclease; Angiogenesis;
Protein synthesis inhibitor; Signal; Pyrrolidone carboxylic acid.
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developmentally regulated genes when expressed in NIH 3T3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-FEB-2003 (Rel. 41, Last annotation
Angiogenin-related protein precursor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein gene and two pseudogenes.";
Genomics 29:200-206(1995).
                                    Mol. Cell. Biol. 17:1503-1512(1997)
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121 KDFRYIVIACEDGWPVHF 138
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PEam; PE00074; rnaseA; 1.
PRINTS; PR00794; RIBONUCLEASE.
ProDom; PD000535; RNaseA; 1.
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                                                                                                                                                                                                                                                                                                             EMBL; U72672; AAC05794.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                SM00092; RNAse Pc;
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MGD; MGI:1201793; Angl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANGR MOUSE
Q64438;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1997
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                                                                                        between the Swiss institute. There are no restriction way the European Bioinformatics Institute. There are no restriction way use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial modified and this statement is not removed. Waww.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33 CKRVNTFIISSATTVKAIC---IGVINMNV-LSTTRFQLNTCTRTSITPR-PCPYSSRTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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"The amino acid sequence of pike-whale (lesser-rorqual) pancreatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Cetartiodactyla, Cetacea, Mysticeti,
Balaenopteridae, Balaenoptera.
NCBL_TAXID=9767;
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-!- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside phosphates and 3'-phosphooligonucleotides ending in C-P or with 2',3'-cyclic phosphate intermediates.
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Pancreas.
-!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
SIMILARITY: Belongs to the pancreatic ribonuclease family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ANGIOGENIN-RELATED PROTEIN.
PYRROLIDONE CARBOXYLIC ACID (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-OCT-2003 (Rel. 42, Last annotation update)
Ribonuclease pancreatic (EC 3.1.27.5) (RNase 1) (RNase A)
RNASE1 OR RNS1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Balaenoptera acutorostrata (Minke whale) (Lesser rorqual)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29A6EB814429C4AD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Pred. No. 3.6e-09; 10; Mismatches 28
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BY SIMILARITY.
BY SIMILARITY.
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21-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00127; RNASE_PANCREATIC; 1.
Signal; Hydrolase; Nuclease; Endonuclease;
Pytrolidone carboxylic acid.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 149.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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                                                                                                                                                                                                                                                                                                                                                                           MGD; MGI:104984; Angrp.
InterPro; IPR001477; RNaseA.
Pfam; PF00074; rnaseA; 1.
PRINTS; PR00794; RIBONUCLEASE.
ProDom; PD000535; RNaseA; 1.
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|123 FRYIIIGCENGWPVHF 138
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1 QNWATFQQKHIINT-PIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NMN 58
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 -!- FUNCTION: Basic protein with antiproliferative/cytotoxic activity against several tumor cell lines in vitro, as well as antitumor in vivo. It exhibits a ribonuclease-like activity against high molecular weight ribosomal RNA.
                                                    -!- DEVELOPMENTAL STAGE: Early embryos (up to four blastomere stage).
-!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
PDB; 10NC; 31-JAN-91.
InterPro; 17R001427; RNaseA.
Pfam; PF00074; rnaseA; 1.
ProDom; PD0000535; RNaseA; 1.
ProDom; PR000052; RNase P; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANGS OR ANGL.
Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
r (EC 3.1.27.-) (Angiogenin-related protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VLTTSEFYLSDC---NVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 104;
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                                                                                                                                                                                        PYRROLIDONE CARBOXYLIC ACID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11845 MW; 22A753C2F9E566B4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1;
                                                                                                                                    SMART; SM00092; RNASe Pc; 1.
PROSITE; PS00127; RNASE PANCREATIC; 1.
Hydrolase; Nuclease; Endonuclease; 3D-structure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 4.5e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      49.5%; Pred. ....
tive 15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   145 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             46.1%; Score 277.5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=BALB/c;
MEDLINE=97184476; PubMed=9032278;
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01-NOV-1997 (Rel. 35, Last seq
28-FEB-2003 (Rel. 41, Last ann
                                                                                                                                                                            Pyrrolidone carboxylic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                       Query Match
Best Local Similarity
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ACT_SITE
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                                                                                                                                                                                                                                                                                                                                                                                                      1 ONWAKFKEKHIRSTSSIDCNTIMDKAIYIVGGKCKERNTFIISSEDNVKAICSGVSPDRK 60
                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Comparative molecular modeling and crystallization of P-30 protein: a novel antitumor protein of Rana pipiens occytes and early
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=94166079; PubMed=8120892;
Mosimann S.C., Ardelt W., James M.N.G.;
"Refined 1.7 A X-ray crystallographic structure of P-30 protein, an
amphibian ribonuclease with anti-tumor activity.";
J. Mol. Biol. 236:1141-1153(1994).
         -!- CATALYTIC ACTIVITY: Endomucleolytic cleavage to mucleoside 3'-phosphates and 3'-phosphooligonucleotides ending in C-P or U-P with 2',3'-cyclic phosphate intermediates.
-!- SUBCELLUIAR LOCATION: Secreted.
-!- SUBCELLUIAR LOCATION: Parceted.
-!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
PIR, JX0085; JX0085.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              occytes and early embryos. Homology to pancreatic ribonucleases."; J. Biol. Chem. 266:245-251(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-FEB-1994 (Rel. 28, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
29-FCB-2003 (Rel. 41, Last annotation update)
8-30 protein (RC 3.1.27.-) (Onconase).
Rana pipiens (Northern leopard frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Rana.
                                                                                                                                                                                                                                                                                                                                                                                                                                  59 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                   2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=91093131; PubMed=1985896;
Ardelt W., Mikulski S.M., Shogen K.;
"Amino acid sequence of an anti-tumor protein from Rana pipiens
                                                                                                                                                                          Hydrolase, Nuclease, Endonuclease, Pyrrolidone carboxylic acid.
MOD_RES 1 1 PYROLIDONE CARBOXYLIC ACID.
ACT_SITE 10 BY SIMILARITY.
ACT_SITE 35 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3D-STRUCTURE MODELING.
MEDLINE=93066156, PubMed=1438177,
Mosimann S.C., Johns K.L., Ardelt W., Mikulski S.M., Shogen K.,
                                                                                                                                                                                                                                                                                                                            Length 111;
                                                                                                                                                                                                                                                                                                                                                  27; Indels
                                                                                                                                                                                                                                                                                                 D64BA72456C10788 CRC64;
                                                                                                                                                                                                                                                                                                                         Score 374; DB 1;
Pred. No. 2.1e-33;
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                                                                                         HSSP; P11916; 1BC4.
InterPro; IPR001427; RNaseA.
Pfam; PF00074; TRASEA; 1.
ProDon; PD00535; RNaseA; 1.
SMART; SM0092; RNASe Pc; 1.
PROSITE; PS00127; RNASE PANCREATIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS).
                                                                                                                                                                                                                                                                                                12461 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Rel. 19, Created)
(Rel. 28, Last seq
 Biochem. 106:729-735(1989)
                                                                                                                                                                                                                                                                                                                          62.1%;
65.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proteins 14:392-400(1992).
                                                                                                                                                                                                                                                                                                                                                    73; Conservative
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35
104
72
82
                                                                                                                                                                                                                                                                                                 111 AA;
                                                                                                                                                                                                                                                                                                                                       Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               James M.N.G.;
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01-FEB-1994
28-FEB-2003
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9; Gaps

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QNWATFQQKHIINTFII-CNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNV
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residues with a 3'flanking guanine. Hydrolyzes poly(U) and poly(C) as substrates, and prefers the former. The S-lectins in frog eggs may be involved in the fertilization and development of the frog embryo. This lectin agglutinates various animal cells, including
                                                                                                                                                                                                                                                                                                                 SMART; SM00092; RNASE PC; 1.
PROSITE; PS00127; RNASE PANCREATIC; 1.
Hydrolase; Nuclease; Endonuclease; Sialic acid; Lectin; 3D-structure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                               normal lymphocytes, erythrocytes, and fibroblasts of animal and human origin. It is cytotoxic against several tumor cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1;
                                                                                   SUBCELLULAR LOCATION: Secreted.
SIMILARITY: Belongs to the pancreatic ribonuclease family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 591.5; DB 1; Length 133; Pred. No. 1.1e-56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RIBONUCLEASE, OOCYTES.
PYRROLIDONE CARBOXYLIC ACID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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129
14762 MW; A7D62594F7D16F0C CRC64;
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SIGNAL 1
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                                                                                                                                                                                                                         EMBL, AF039104, AAD10702.1; -. PIR, A27121, A27121
PDB, 1BC4; 28-OCT-98.
PDB, 1M07; 21-JAN-03.
                                                                                                                                                                                                                                                                                        Pfam; PF00074; rnaseA; 1.
ProDom; PD000535; RNaseA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98.3%;
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                                                                          SUBUNIT: Monomer
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ID LECS RANJA

AC P18839;

DT 01-NOV-1990

DT 01-FEB-1994

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Last sequence update)
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(Rel. 16, (Rel. 28, 1)

01-NOV-1990 01-FEB-1994 10-OCT-2003

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 QNWAKFQEKHIPNISNINCNIIMDKSIYIVGGQCKERNTFIISSATIVKAICSGASTNRN
                                                                                                                                                                                                         FUNCTION: The S-lectins in frog eggs may be involved in the fertilization and development of the frog embryo. This lectin preferentially agglutinate a large variety of tumor cells, but it does not agglutinate non-transformed cells and erythrocytes. SUBUNIT: Moroomet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nitta R., Katayama N., Okabe Y., Iwama M., Watanabe H., Abe Y., Okazaki T., Ohgi K., Irie M.;
"Primary structure of a ribonuclease from bullfrog (Rana catesbelana)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                       Kamiya Y., Oyama F., Oyama R., Sakakibara F., Nitta K., Kawauchi H., Takayanagi Y., Titani K.,
                                                                                                                                                                    'Amino acid sequence of a lectin from Japanese frog (Rana japonica)
Sialic acid-binding lectin (EC 3.1.27.-).
Rana japonica (Japanese reddish Erog).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
NCBI_TaxID=8400;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 VLSTTRFQLNTCIRSATAPRPCPYNSRTETNVICVKCENRLPVHFAGIGRC 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5;
                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: Secreted.
SIMILARITY: Belongs to the pancreatic ribonuclease family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             PYRROLIDONE CARBOXYLIC ACID.
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12326 MW; FDEBDDF3834ED679 CRC64;
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Pred. No. 4.1e-42;
7; Mismatches 15;
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01-FEB-1994 (Rel. 28, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Pabonus-lease, liver (EC 3.1.27.5).
Rana catesbeiana (Bull frog).
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ProDom; PD000535; RNaseA; 1.
SMART; SM00092; RNASe Pc; 1.
PROSITE; PS00127; RNASE PANCREATIC; 1.
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MEDLINE=90130374; PubMed=2613682;
                                                                                                         TISSUE=Egg;
MEDLINE=91035319; PubMed=2229005;
                                                                                           SEQUENCE, AND DISULFIDE BONDS.
                                                                                                                                                                                                  Biochem. 108:139-143(1990)
                                                                                                                                                                                                                                                                                                                                                     interPro; IPR001427; RNaseA.
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HSSP; P11916; 1BC4.
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                                                         NCBI_TaxID=8402;
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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
                Copyright
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- protein search, using sw model OM protein

7, 2004, 21:30:40 ; Search time 5.55659 Seconds (without alignments) 1030.796 Million cell updates/sec May Run on:

US-09-961-400-15

602 Perfect score:

1 QNWATFQQKHIINTPIICNT.....ICVKCENQYPVHFAGIGRCP 110 Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

141681 seqs, 52070155 residues Searched:

141681 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 2000000000 Minimum DB Maximum DB

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

SwissProt 42:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	P11916 rana catesb	9 rana	6 rana	9 rana	2 mus m	mus	bala		pog	7.1			63				-			Q8wn66 cercopithec		P00676 myocastor c	P00683 mus musculu	Q8wn61 aotus trivi	Q8wn67 pongo pygma	9	P00679 cavia porce	Q8wn62 saguinus oe		0	P04059 proechimys	P15467 bos taurus	Q8wn63 macaca mula
SUMMARIES	ID	RNPO RANCA	LECS RANJA	RNPL_RANCA	RN30 RANPI	ANG3 MOUSE	ANGR MOUSE	RNP BALAC	ANGI MOUSE	RNBR_BOVIN	RNP_FIG	RNP_IGUIG	RNBR_CAPCA	ANG2_BOVIN		RNBR_AXIPR	ANGI_SAISC	ANGI MIOTA	RNBR SHEEP	RNP_ANTAM	ANGI_CERAE	RNP_MACRU	RNP MYOCO	RNP_MOUSE	ANGI_AOTTR	ANGI PONPY	ANGI_PIG	RNPB CAVPO	ANGI SAGOE	RNP_HORSE	RNP_CAMDR	RNP PROGU	RNS4_BOVIN	ANGI_MACMU
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₩	Query Match	98.3	75.6	62.1	46.1	25.7	24.8	22.5	22.5	22.2	22.0	21.8	21.3	21.2	21.2	21.2	20.8	20.6	20.5	20.3	20.3	20.3	20.0	20.0	19.9	6.61	19.9	19.7	19.6	19.5	19.4	19.4	19.2	19.2
	Score	91.	455	374	277.5	154.5	149.5	135.5	135.5	133.5	132.5	131.5	128.5	127.5	127.5	127.5	125	124	123.5	122.5	122.5	122	120.5	120.5	120	120	119.5	118.5	118		116.5		'n.	115.5
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P10152 bos taurus P00666 rangifer ta Q8wn64 papio hamad P03950 homo sapien	Q8wme8 pan troglod P00664 capreolus c P00662 giraffa cam	Q9jjhl mus musculu P31347 oryctolagus P24717 cricetulus	O55004 rattus norv Q9wtt5 acomys cahi
ANGI BOVIN RNP RANTA ANGI PAPHA ANGI HUMAN	ANGI_PANTR RNP_CAPCA RNP_GIRCA	RNS4 MOUSE ANGI_RABIT RNP CRILO	RNS4 RAT RNP_ACOCA
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148 124 146	147 124 124	148 125 130	147
18.9 18.9 18.9	18.8 18.7 18.7	18.7 18.6 18.5	18.5
113.5 113.5 113.5	113 112.5 112.5	112.5 112 111.5	111.5
33 36 36 7	38 39 40	41 42 43	44

ALIGNMENTS

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STRUCTURE BY NMR OF 23-133.

MEDLINE=98437383; PubMed=9761686;

Chang C.-F., Chen C., Chen Y.-C., Hom K., Huang R.-F., Huang T.H.;

"The solution structure of a cytotoxic ribonuclease from the oocytes of Rana catesbeiana (bullfrog) ";

J. Mol. Biol. 283:231-244(1998).

-!- FUNCTION: Preferentially cleaves single-stranded RNA at pyrimidine
   P119<u>T6; Q9PWR7; Created)</u>
10-OCT-1989 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
110-OCT-2003 (Rel. 42, Last annotation update)
Ribonuclease, oocytes precursor (EC 3.1.27.-) (RC-RNase) (Sialic acid-binding lectin) (SBL-C).
                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Egg;
MEDLINE=8729649; PubMed=3304421;
Titani K., Takio K., Kuwada M., Nitta K., Sakakibara F., Kawauchi H.,
Takayanagi G., Hakomori S.;
"Amino acid sequence of sialic acid binding lectin from frog (Rana cateabeiana) eggs."
Biochemistry 26:2189-2194 (1987).
                                                                                                                                                                                                                                                        MEDLINE-98162825; PubMed=9497370;
MEDLINE-9816825; PubMed=9497370;
Huang H.C., Wang S.C., Leu Y.U., Lu S.C., Liao Y.D.;
"The Rana catesbeiana rcr gene encoding a cytotoxic ribonuclease.
Tissue distribution, cloning, purification, cytotoxicity, and active residues for RNase activity.";
                                                                                                                                 Rana catesbeiana (Bull frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
NCBI_TaxID=8400;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Liao Y.-D.;

"A pyrimidine-quanine sequence-specific ribonuclease from Rana catesbeiana (bullfrog) occytes.";

Nucleic Acids Res. 20:1371-1377(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUB=Egg;
MEDL.INE=93152604; PubMed=8448385;
Nitta K., Oyama F., Oyama R., Sekiguchi K., Kawauchi H.,
Takayanagi Y., Hakomori S., Titani K.;
"Ribonuclease activity of sialic acid-binding lectin from Rana
133 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHARACTERIZATION, AND SEQUENCE OF 81-101.
MEDLINE-92220613; PubMed=1373237;
 PRT;
                                                                                                                                                                                                                                                                                                                                      residues for RNase activity.";
J. Biol. Chem. 273:6395-6401(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    catesbelana eggs.";
Glycobiology 3:37-45(1993).
STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 23-133.
                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                               TISSUE=Liver;
 RANCA
RNPO
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us-09-961-400-15.rpr

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NRGPB
PAGCEASTLY 15
NRGPB
NAALCEATAGE NAMES IB
C; Species: Cavia porcellus (guinea pig)
C; Species: Cavia porcellus (guinea pig)
C; Species: Cavia porcellus (guinea pig)
C; Species: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 31-Mar-2000
C; C; Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 31-Mar-2000
C; C; Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 31-Mar-2000
C; Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 31-Mar-2000
C; Date: 25-Apr-1982
R; Van den Berg, A.; Van den Hende-Timmer, L.; Hofsteenge, J.; Gaastra, W.; Beintema, J.J
A; Title: Guinea pig pancreatic ribonucleases. Isolation, properties, primary structure a A; Reference number: A91247; MULD: 77185023; PMID: 862624
A; Molecule type: protein
A; Residues: 1-128 < VAN>
A; Note: 64-Pro was also found
C; Superfamily: pancreatic ribonuclease
C; Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
C; Superfamily: pancreatic ribonuclease
C; Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F; 12, 41, 119/Active site: His, Lys, His #status predicted
F; 21, 34/Binding site: carbohydrate (Asn) (covalent) #status experimental
F; 26-84, 40-95, 58-110, 65-72/Disulfide bonds: #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CKRVNTFIISSATTVKAICTG----VINMNVLSTTRFQLNTCTRTSITPR-PCPYSSRTE 87
                                        | | | | | | | : | | | | : | | | | : | | | | CKEVNTFIHGTRNDIKAICNDKNGEPYNNFRRSKSPFQITTCKHKGGSNRPPCGYRAIAG 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----STTRPQLNTCTRTSITPRP-CPYSSRTEINYICVKCENQ--YPVHF 103
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                                                                                                                                                 88 TNYICVKCENOYPVHF 103
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A; Cross-references: GB:M27814; NID:g200762; PIDN:AAA40060.1; PID:g200763
A; Cross-references: GB:M27814; NID:g200762; PIDN:AAA40060.1; PID:g200763
R; Samuelson, L.(.) Miebauer, K.; Howard, G.; Schmid, R.M.; Koeplin, D.; Meisler, M.H.
R; Samuelson, L.(.) Mebauer, E935-6941, 1991
A; Title: Isolation of the murine ribonuclease gene Rib-1: structure and tissue specific A; Reference number: S22598; MUID:92107684; PMID:1840677
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---STTRFQLNTCTRTSITPRP-CPYSSRTEINYICVKCE-NQY-PVHF 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     89 TCKNRKSNCYKSSSALHITDCHLKGNSKYPNCDYKTTQYQKHILVACEGNPYVPVHF 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              angiogenin - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
                                 Danctreatic ribonuclease (EC 3.1.27.5) precursor - mouse
NyAlternate names: RNase 1; RNase A
Cispecies: Mus musculus (house mouse)
Cispecies: Mus musculus (house mouse)
Cispecies: Nuov-1980 #sequence revision 13-Mar-1997 #text_change 18-Jun-1999
Cisacession: A34090; 822598; A00830
Rischueller, C.; Nijssen, H.M.J.; Kok, R.; Beintema, J.J.
Mol. Biol. Evolution of nucleic acids coding for ribonucleases: the mRNA seque A; Reference number: A34090; MUID:90136034; PMID:2299980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33 FORQHMDPDGSSINSPTYCNOMMKRR-DMTNGSCKPVNTFVHEPLADVQAVCS---QENV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:X60103; NID:953981; PIDN:CAA42697.1; PID:953982 R;Lenstra, J.A.; Beintema, J.J. Bur. J. Biochem. 98, 399-408, 1979 A;Title: The amino acid sequence of mouse pancreatic ribonuclease. A;Reference number: A00830; MUID:80024269; PMID:556267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Note: this sequence was submitted to the Protein Sequence Database, C;Superfamily: pancreatic ribonuclease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ري
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R;Bond, M.D.; Strydom, D.J.; Vallee, B.L.
Blochim, Biophys. Acta 1162, 177-186, 1993
A;Title: Characterization and sequencing of rabbit, pig
A;Reference number: $29833; MUID:93192291; PMID:8448182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 119.5; DB 1;
Pred. No. 6.5e-05;
6; Mismatches 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20.0%; Score 120.5; DB 1, 30.8%; Pred. No. 6.3e-05; ive 16; Mismatches 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19.9%;
39.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 30; Conserv
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A;Molecule type: DNA
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Matches
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Biochim. Blophys. Acta 453, 400-409, 1976
Biochim. Blophys. Acta 453, 400-409, 1976
A; Title: Isolation, properties and primary structure of coypu and chinchilla pancreatic A; A; Reference number: A90612; MUID: 77065676; PMID: 99896
A; Recession: A00822
A; Molecule type: protein
A; Molecule type: protein
C; Keywords: 1128 < VAN>
C; Superfamily: pancreatic ribonuclease
C; Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
C; Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
C; Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
C; Keywords: glycoprotein; hydrolase; mucleic acid digestion; pancreas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65
                                                                                                   62 NVACKNGQINCYQSYSTMSIIDCREIGSSKYPNCAXKTIQAKKHIIVACEGNFYVPVHY 120
AKFERQHIDSNPSSVSSSNYCNQMMKSR-NLTQGRCKPVNTFVHESLADVQAVCS---QK 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64 LCKNGQTNCYQSNSNMHITDCRVTSNSDYPNCSYRTSQEEKSIVVACEGNPYVPVHF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pandreatic ribonuclease (EC 3.1.27.5) - nutria (tentative sequence)
N;Alternate names: RNase 1; RNase A
C;Species: Myodastor coypus (nutria, coypu)
C;Date: 24-Apr-1984 #sequence_revision 30-Sep-1988 #text_change 31-Mar-2000
C;Accession: A00822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -STIRFQLNICIRISIIPRP-CPYSSRIEINYICVKCE-NQY-PVHF 103
                                                                                                                                                                                                                                                                               pancreatic ribonuclease (EC 3.1.27.5) - red kangaroo
N;Alternate names: RNase 1; RNase A
C;Species: Macropus rufus, Megaleia rufa (red kangaroo)
C;Date: 30-Nov-1980 #sequence_revision 30-Nov-1980 #text_change 04-Oct-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 FOROHMDIEHSTASSSNYCNLMMKAR-DMTSGRCKPLNTFIHEPKSVVDAVCHQENVTCK
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                                                              STTRFQLNTCTRTSITPRP-CPYSSRTETNYICVKCE-NQY-PVHF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: protein
A;Residues: 1-122 <GAA>
C;Superfamily: pancreatic ribonuclease
C;Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F;11,40,117/Active site: His, Lys, His #status predicted
F;25-83,39-94,57-109,64-71/Disulfide bonds: #status predicted
F;61/Binding site: carbohydrate (Asn) (covalent) #status absent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   52 TGVINMAVLSTTRFQLNTCTRISITPRP-CPYSSRTETNYICVKCENQY-PVHF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66 NGRINC-YKSNSRLSIINCRQIGASKYPNCQYETSNINKQIIVACEGQYVPVHF
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                                                                                                                                                                                                                                                                                                                                                                                                                       C;Accession: A00833
R;Gastra, W.; Welling, G.W.; Beintema, J.J.
Eur. J. Biochem. 86, 209-217, 1978
A;Title: The amino-acid sequence of Kangaroo pancreatic ribonuclease.
A;Reference number: A00833; MUID:78190621; PMID:658039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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30.7%; Pre
tive 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35; Conservative
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Best Local Similarity
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                                                                        58 NVL----
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Gaps

17;

Indels

42; DB 1;

Length 124;

28

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--ICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINM 57
   C;Keywords: glycoprotein; hydrolase; mucleic acid digestion; pancreas F;12,41,119/Active site: His, Lys, His #status predicted F;21.34,76/Binding site: carbohydrate (Asn) (covalent) #status experimental F;26-84,40-95,58-110,65-72/Disulfide bonds: #status experimental
                                                                                                                                                                                                                                                                                                                                        6 FOOKHI-----INTPILCUTIMDNNIYIVGGOCKRVNTFIISSATTVKALCTGV-INMN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59 VLSTTRFQLNT-----CTRISITPRP-CPYSSRTEINYICVKCENQ--YPVHF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67 NGOTNCYQSNSTMHITDCRQTGSSKYPNCAYKASQEQKHİIVACEGNPPVPVHF
                                                                                                                                                                                                     22.0%; Score 132.5; DB 1
31.6%; Pred. No. 3.3e-06;
                                                                                                                                                                                                                        31.6%; Pred. ...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-119 <ZHA>
C;Superfamily: pancreatic ribonuclease
                                                                                                                                               Query Match
Best Local Similarity 5..
Local 36; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 35; Conserv
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                          A)Cross-references: EMBL:X59767; NID:g150; PIDN:CAA42439.1; PID:g151
R;Watanabe, H.; Katch, H.; Ishii, M.; Komoda, Y.; Sanda, A.; Takizawa, Y.; Ohgi, K.; Iri
J. Biochem. 104, 939-945, 1988
A;Title: Primary structure of a ribonuclease from bovine brain.
A;Reference number: JX0056; MUID:89214015; PMID:3243767
                                                                                                                                                                                     M.; Palmieri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    88
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A;Residues: 1,'Q',3-124 <JAC>
R;Weiernga, R.K.; Huizinga, J.D.; Gaastra, W.; Welling, G.W.; Beintema, J.J.
FEBS Lett. 31, 181-185, 1973
A;Title: Affinity chromatography of porcine pancreatic ribonuclease and reinvestigation
pancreatic-type ribonuclease (EC 3.1.27.5) BRb precursor, brain - bovine (Species: Bos primigenius taurus (cattle) C'Species: Las primigenius taurus (cattle) C'Species: 22-Nov-1993 #sequence_revision 12-May-1995 #text_change 22-Jun-1999 C'Saccession: S20066; JX0056 HS (Confalone, E.; Cosi, C.; Sorrentino, S.; Viola, M.; Palmie: Nucleic Acids Res. 19, 6469-6474, 1991 A; Title: Molecular cloning of the gene encoding the bovine brain ribonuclease and its is a seference number: S20066; MUID:92093604; PMID:1754384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ď
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A.Residues: 1-124 <MIE>
A.Residues: 1-124 <MIE>
B.Phelan, J.J.; Hirs, C.H.W.
J. Biol. Chem. 245, 654-661, 1970
A.Title: The primary structure of porcine pancreatic ribonuclease. III. The disulfide A.Reference number: A92072; MUID:70104198; PMID:4904878
A.Contents: annotation; disulfide bonds
C.Superfamily: pancreatic ribonuclease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---STIRFQLNTCTRISITPRP-CPYSSRIEINYICVKCE-NOY-PVHFA 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 ATFQQKHI-----INTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINM 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pancreatic ribonuclease (EC 3.1.27.5) - pig
N.Alternate names: RNase 1; RNase A
N.Alternate names: RNase 1; RNase A
C.Species: Sus scrofa domestica (domestic pig)
C.Date: 24-Apr-1984 #sequence revision 24-Apr-1984 #text_change 03-Jun-1994
C.Accession: A92071; A91391; \( \bar{A}\) \( \bar{A}\) \( \bar{A}\) \( \bar{A}\) \( \bar{A}\) \( \bar{A}\) \( \bar{A}\) \( \bar{A}\) \( \bar{A}\) \( \bar{A}\) \( \bar{A}\) \( \bar{A}\) \( \bar{A}\) \( \bar{A}\) \( \bar{A}\) \( \bar{A}\) \( \bar{A}\) \( \bar{A}\) \( \bar{A}\) \( \bar{A}\) \( \bar{A}\) \( \bar{A}\) \( \bar{A}\) \( \bar{A}\) \( \bar{A}\) \( \bar{A}\) \( \bar{A}\) \( \bar{A}\) \( \bar{A}\) \( \bar{A}\) \( \bar{A}\) \( \bar{A}\) \( \bar{A}\) \( \bar{A}\) \( \bar{A}\) \( \bar{A}\) \( \bar{A}\) \( \bar{A}\) \( \bar{A}\) \( \bar{A}\) \( \bar{A}\) \( \bar{A}\) \( \bar{A}\) \( \bar{A}\) \( \bar{A}\) \( \bar{A}\) \( \bar{A}\) \( \bar{A}\) \( \bar{A}\) \( \bar{A}\) \( \bar{A}\) \( \bar{A}\) \( \bar{A}\) \( \bar{A}\) \( \bar{A}\) \( \bar{A}\) \( \bar{A}\) \( \bar{A}\) \( \bar{A}\) \( \bar{A}\) \( \bar{A}\) \( \bar{A}\) \( \bar{A}\) \( \bar{A}\) \( \bar{A}\) \( \bar{A}\) \( \bar{A}\) \( \bar{A}\) \( \bar{A}\) \( \bar{A}\) \( \bar{A}\) \( \bar{A}\) \( \bar{A}\) \( \bar{A}\) \( \bar{A}\) \( \bar{A}\) \( \bar{A}\) \( \bar{A}\) \( \bar{A}\) \( \bar{A}\) \( \bar{A}\) \( \bar{A}\) \( \bar{A}\) \( \bar{A}\) \( \bar{A}\) \( \bar{A}\) \( \bar{A}\) \( \bar{A}\) \( \bar{A}\) \( \bar{A}\) \( \bar{A}\) \( \bar{A}\) \( \bar{A}\) \( \bar{A}\) \( \bar{A}\) \( \bar{A}\) \( \bar{A}\) \( \bar{A}\) \( \bar{A}\) \( \bar{A}\) \( \bar{A}\) \( \bar{A}\) \( \bar{A}\) \( \bar{A}\) \( \bar{A}\) \( \bar{A}\) \( \bar{A}\) \( \bar{A}\) \( \bar{A}\) \( \bar{A}\) \( \bar{A}\) \( \bar{A}\) \( \bar{A}\) \( \bar{A}\) \( \bar{A}\) \( \bar{A}\) \( \bar{A}\) \( \bar{A}\) \( \bar{A}\) \( \bar{A}\) \( \bar{A}\) \( \bar{A}\) \( \bar{A}\) \( \bar{A}\) \( \bar{A}\) \( \bar{A}\) \( \bar{A}\) \( \bar{A}\) \( \bar{A}\) \( \bar{A}\) \( \bar{A}\) \( \bar{A}\) \( \bar{A}\) \( \bar{A}\) \( \bar{A}\) \( \bar{A}\) \( \bar{A}
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F,88/Binding site: carbohydrate (Asn) (covalent) #status experimental F;155/Binding site: carbohydrate (Thr) (covalent) #status experimental F;159/Binding site: carbohydrate (Ser) (covalent) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2; Length 167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A.Molecule type: protein
A.Residues: 27-154, '8', 156-166 < WAT>
A.Residues: 27-154, '8', 156-166 < WAT>
A.Residues: 27-154, '8', 156-166 < WAT>
C.Superfamily: pancreatic tribonuclease
C.Reywords: glycoprotein; hydrolase
F:38,67,145/Active site: His, Lys, His #status predicted
F:210,66-121,84-136,91-98/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 133.5; DB 2
Pred. No. 3.6e-06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22.2%;
31.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      38; Conservative
                                                                                                                                                                                                                                                                                                         A,Accession: S20066
A,Molecule type: DNA
A,Residues: 1-167 <SAS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 38; Conservations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: JX0056
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A, Title: Primary structure of pronghorn pancreatic ribonuclease: close relationship betu
A, Reference number: A00813; MUID:80075014; PMID:513141
C;Species: Iguana iguana (common iguana)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 21-Aug-1998
C;Accession: S41111
Eur. J. Beintema, J.J.; Hofsteenge, J.
Bur. J. Blochem. 219, 641-646, 1994
A;Title: The amino acid sequence of iguana (Iguana iguana) pancreatic ribonuclease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NyAlternate names: RNase 1; RNase A. C.Species: Antilocapra americana (pronghorn)
C;Species: Antilocapra americana (pronghorn)
C;Accession: A00813
R;Beintema, J.J.; Gaastra, W.; Munniksma, J.
J. Mol. Evol. 13, 305-316, 1979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 QNWATFQQKHI-----INTPLICNTIMDNNIYIVGGQCKRVNTFLISSATTVKAIC--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              52 --TGVINMNVLSTTRFQLNTCTRISIT-PRPCPYSSRIETNYICVKCENQYPVHF 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60 GGTHYEDNLYDSNESFDLTDCKNVGGTAPSSCKYNGTPGTKRIRIACENNQPVHF 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pancreatic ribonuclease (EC 3.1.27.5) - pronghorn (tentative sequence)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A.Residues: 1-124 < BEI>
C.Superfamily: pancreatic ribonuclease
C.Keywords: glycoprotein; hydrolase; muleic acid digestion; pancreas
C.Keywords: glycoprotein; hydrolase; muleic acid digestion; pancreas
C.Keywords: glycoprotein; hydrolase; muleic acid digestion; pancreas
F.12, 41,119/Active site: His, Lys, His #status predicted
F.26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                  Length 119;
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                                                                                                                                                                                                                                                                                                                                                                                                                     .5;
.4e-06;
51;
                                                                                                                                                                                                                                                                                                                                                                                                               DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                         21.8%; Score 131.5;
30.4%; Pred. No. 4e-(ive 16; Mismatches
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pancreatic ribonuclease.

experimental

pancreas

7;

23;

DB 1; Length 124;

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Aymolecule type: DNA
A,Molecule type: DNA
A,Molecule type: DNA
A,Molecule type: DNA
A,Residues: 1-145 < BON>
A,Cross-references: GB:U22516; NID:g726325, FIDN:AAA91366.1; FID:g726326
C,Genetics:
A,Introns: #status absent
C,Function: hydrolyzes tRNA; induces vascularization of normal and malignant tissues
A,Description: hydrolyzes tRNA; induces vascularization of normal and malignant tissues
C,Superfamily: pancreatic ribonuclease
C,Superfamily: pancreatic ribonuclease
C,Superfamily: pancreatic ribonuclease
F,124/Domain: signal sequence #status predicted <SIG>
F,25-145/Product: angiogenesis; hydrolase; nucleic acid (SIG)
F,125-Modified site: pyrrolidone carboxylic acid (ANT)
F,135/Modified site: pyrrolidone carboxylic acid (ANT)
F,137/Active site: His, Lys, His #status predicted
F,50-104,63-115,81-130/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FQQKHII-----NTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNV 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8 FORQHMDSGNSPGNNPNYCNOMMARR-KMTQGRCKPVNTFVHESLEDVKAVCS---QKNV 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Anglogenin precursor - mouse anglogenesis factor
NyAlternate names: anglogenesis factor
NyContains: ribonuclease (EC 3.1.27.-)
Cypecies: Mus musculus (house mouse)
Cypecies: Mus musculus (house mouse)
Cypecies: Musculus (house mouse)
Cypecies: Musculus (house mouse)
Cypecies: Musculus (house mouse)
Cypecies: Musculus (house mouse)
Cypecies: Musculus (house mouse)
Cypecies: Musculus (house mouse)
Cypecies: Musculus (house mouse)
AyTitle: Isolation and sequencing of mouse anglogenin DNA.
AyReference number: A35932; MUID:91025023; PMID:2222458
AyReference number: A35932
AyStatus: not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64 LCKNGRINCYBSNSTMHITDCRQTGSSKYPNCAYKTSQKEKHIIVACEGNPYVPVHF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60 L-----STTREQLNTCTRISITPRP-CPYSSRTEINYICVKCE-NQY-PVHF 103
     N,Alternate names: RNase 1; RNase A
C;Species: Balaenoptera acutorostrata (minke whale, lesser rorqual)
C;Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 03-Jun-1994
                                                                                                                                                                                                                                                                              A;Residues: 1-124 <EMM>
C;Superfamily: pancreatic ribonuclease
C;Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancre
C;Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancre
F;12,41,119/Active site: His, Lys, His #status predicted
F;26-84,40-95,88-110,65-72/Disulfide bonds: #status predicted
F;76/Binding site: carbohydrate (Asn) (covalent) (partial) #status
                                                                             C;Accession: A00818
C;Accession: Melling, G W.; Beintema, J.J.
R;Emmens, M.; Welling, G W.; Beintema, J.J.
Biochem. J. 157, 317–323, 1976
A;Title: The maino acid sequence of pike whale (lesser rorqual)
A;Reference number: A00818; WUID:76277855; PMID:962870
A;Reference rype: protein
A;Rolecule type: protein
A;Residues: 1-124 < EPMA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                              22.5%; Score 135.5; DB 1
33.3%; Pred. No. 1.7e-06;
iive 16; Mismatches 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               88 TNYICVKCENQYPVHF 103
RNase 1; RNase
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 39; Conserv
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C;Species: Rana pipiens (northern leopard frog)
C;Date: 31-Jul-1991 #sequence_revision 31-Jul-1991 #text_change 30-Jun-1993
C;Accession: A3035
E;Ardelt, W.; Mikulski, S.M.; Shogen, K.
J. Biol. Chem. 266, 245-251, 1991
A;Title: Amino acid sequence of an anti-tumor protein from Rana pipiens oocytes and earl A;Reference number: A39035; MUID:91093131; PMID:1985896
                                                                                                                                                                                                                                                                                                                                                                                                                         Opd
                                                                                                                                                                                                                                                                                                                                                                                                    C:Accession: JX0085
R;Nitta, R.; Katayama, N.; Okabe, Y.; Iwama, M.; Watanabe, H.; Abe, Y.; Okazaki, T.;
J. Biochem. 106, 729-735, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Rana catesbeiana) liver.
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                                                                                                                                                                                                                                                                                                           puncreatic ribonuclease (EC 3.1.27.5) - bullfrog
C;Species: Rana catesbeiana (bullfrog)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 05-Aug-1994
                                        QNWATFQQKHIINTP-IICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGV-INMN
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C.Keywords: hydrolase; pyroglucamic acid
C.F.Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:10,35,104/Active site: His, Lys, His #status predicted
F:19-72,34-82,52-97,94-111/Disulfide bonds: #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A) Title: Primary structure of a ribonuclease from bullfrog A) Reference number: UX0085, MUID:90130374; PMID:2613682 A) Accession: UX0085
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48.6%; Pred. No. 2.1e-20;
iive 16; Mismatches 32
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Pred. No. 2.9e-30;
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A,Status: preliminary
A,Molecule type: protein
A,Residues: 1-104 <ARD>
C,Superfamily: pancreatic ribonuclease
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Best Local Similarity 65.0%
Local 73; Conservative
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A; Residues: 1-111 <NIT>
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21
Length 145;
                                 Indels
 DB 1;
ch 22.5%; Score 135.5; DB 1; Similarity 39.5%; Pred. No. 2e-06; 30; Conservative 12; Mismatches 29;
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RESULT

- minke whale

pancreatic ribonuclease (EC 3.1.27.5)

NRWHK

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

7, 2004, 21:38:36; Search time 9.98129 Seconds Run on:

(without alignments) 1060.090 Million cell updates/sec

US-09-961-400-15

Perfect score:

602 1 QNWATFQQKHIINTPIICNT.....ICVKCENQYPVHFAGIGRCF 110 Seguence:

BLOSUM62 Scoring table:

Gapop 10.0 , Gapext 0.5

283366 seqs, 96191526 residues Searched:

Total number of hits satisfying chosen parameters: Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR 78:*
1: Pir1:*
2: pir2:*
3: pir3:*
4: pir4:* 2 8 4

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

pancreatic ribonuc anglogenin precurs pancreatic ribonuc anglogenin - rabbi pancreatic ribonuc pancreatic ribonuc pancreatic ribonuc pancreatic ribonuc pancreatic ribonuc pancreatic ribonuc ribonuclease-relat pancreatic ribonuc ribonuclease-relat angiogenin precurs pancreatic-type ri pancreatic ribonuc pancreatic ribonuc pancreatic ribonuc pancreatic ribonuc angiogenin - pig pancreatic ribonuc pancreatic ribonuc pancreatic ribonuc pancreatic ribonuc pancreatic ribonuc pancreatic ribonuc angiogenin [valida ribonuclease Description SUMMARIES A27121 JX0120 JX0085 A39035 A39035 NRWHK A35932 S20066 B43825 S22808 NRBOB a Query Match Length DB 44.00 199.5 44.4 44.6 199.5 5 199.5 6 Score 588.5 455 133.5 132.5 131.5 122.5 122.5 120.5 120.5 119.5 135.5 135.5 118.5 117.5 116.5 116.5 116.5 116.5 113.5 112.5 112.5 112.5 112 111.5 274.5 Result No.

pancreatic ribonuc pancreatic ribonuc	pancreatic ribonuc pancreatic ribonuc	pancreatic ribonuc pancreatic ribonuc	pancreatic ribonuc	pancreatic ribonuc seminal ribonuclea	bemilial fibonuclea pancreatic ribonuc	pancicatic ribonuc pancreatic ribonuc pancreatic ribonuc
NRWB NREKN	S07141 NRBO 161900	NRSH JX0115	NRCB NRRT	NRHP A47498 NRROS	NRGN NRDEF	S04503 S08546
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124	124 150 158	124 119	154	125 125 150	124	125
18.4 4.8.4	18.4 18.4 4.4	18.2 18.0	18.0	17.7	17.4	17.3
110.5	110.5	109.5	108.5	106.5	104.5	104 103.5
30 31	3 3 3 4 4 4 4	365	38	4 4 1 0 4 1	42	4.4 5

ALIGNMENTS

RESULT A27121	.1
ribonu C;Spec	ribonuclease-related sialic acid-binding lectin - bullfrog C,Species: Rana catesbeiana (bullfrog)
C;Date C;Acce	C;Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 30-Jun-1993 C;Accession: A27121
R, Tita Biocher	R;Titani, K.; Takio, K.; Kuwada, M.; Nitta, K.; Sakakibara, F.; Kawauchi, H.; Tal Biochemistry 26, 2189-2194, 1987
A;Titl(A;Refe	A, Title: Amino acid sequence of sialic acid-binding lectin from frog (Rana catesk A, Reference number: A27121; MUID:87299649; PMID:3304421
A, Molec	A. Molecule type: protein
C; Super	A;kesiques: 1-111 <tit> C:Keywords: 1-011 <tit> C:Keywords: 1-0-1:</tit></tit>
Query	Ouery Match 97.8%; Score 588.5; DB 2; Length 111;
Matches	u Similarity 98.2%; Pred. No. 1.4e-51; 109; Conservative 1; Mismatches 0;
δλ	7.9
qa	
٥٧	60 LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
Db	61 LSTTRFQLNTCTRTSITPRPCPYSSRIEINYICVKCENOYPVHFAGIGRCP 111

kayanac (beiana)

JX0120

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CiSpecies: Rana japonica (Japanese frog)
CiSpecies: Rana japonica (Japanese frog)
CiSpecies: Rana japonica (Japanese frog)
CiSpecies: Rana japonica (Japanese frog)
CiAccession: JAS-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
CiAccession: JAS-143, 1990
RiKamiya, Y.; Oyama, F.; Oyama, R.; Sakakibara, F.; Nitta, K.; Kawauchi, H.; Takayanagi
A; Raference number: JAS-143, 1990
A; Reference number: JAS-143, 1990
CiSpecial type: protein
A; Residues: 1-111 cKAM>
A; Residues: 1-111 cKAM>
C; Superiamily: pancreatic ribonuclease
C; Superfamily: pancreatic ribonuclease
C; Keywords: lectin; pyroglutamic acid
C; Keywords: lectin; pyroglutamic acid
F; 19-72, 34-82, 52-97, 94-111/Disulfide bonds: #status experimental

Gaps 3 Query Match 75.6%; Score 455; DB 1; Length 111; Best Local Similarity 78.4%; Pred. No. 2.6e-38; Matches 87; Conservative 7; Mismatches 15; Indels

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2 EDWLTFQKKHITNTRDVDCDNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN 57
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                                                                                                                                                                                                                        59 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
                                                                                                                                                                                                                                                                                               Length 104;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: Newton, Dianne L.
APPLICANT: Newton, Dianne L.
APPLICANT: Modawer, Alexander
TILLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
                                          /label= Onc
/note= "Onconase from Rana pipiens"
                                                                                                                                                            Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compartible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIAN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,08/875,811
                                                                                                                     45.6%; Score 274.5; DB 2; allarity 48.6%; Pred. No. 1.7e-24; Conservative 16; Mismatches 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16; Mismatches
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APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            UMBER: US/08/875,811
19-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 39, Application US/08875811
Patent No. 6045793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41,739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Faris, Susan K.
REGISTRATION NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 01
TELECOMMULCATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 39:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    105 amino acids
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NAME/KEY: Protein
LOCATION: 1..104
OTHER INFORMATION: /
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Matches 54; Conserv
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Best Local Similarity
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
                                                                                                                                                         54;
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US-08-875-811-39
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1 ONWAIFQOKHIINI-PIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NMN 58

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1 QNWATFQQKHIINT-PIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NMN 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
                            58 VLTTSEFYLSDC---NVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59 VLSTTRFQLNTCTRTSITPRPCPYSSRTEINYICVKCENQYPVHFAGIGRC 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              45.6%; Score 274.5; DB 3; Length 355; 48.6%; Pred. No. 7.7e-24; tive 16; Mismatches 32; Indels 9
                                                                                                                                                                                                                  GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Rybak, Susanna M.

APPLICANT: Newton, Dianne L.

APPLICANT: Noque, Lluis

APPLICANT: Wlodawer, Alexander

TITLE OF INVENTION: Recombinant Ribonuclease Proteins

NUMBER OF SEQUENCES: 64

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                            E: Townsend and Townsend and Crew LLP
Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   015280-244100US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7, 2004, 21:40:45
                                                                                                                                                                        Sequence 41, Application US/08875811 Patent No. 6045793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: FAILS, SUGAN K.
REGISTRATION NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 01:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                       Townsend and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (415) 576-0300 INFORMATION FOR SEQ ID NO: 4 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : 355 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 48.6
Matches 54; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: TWO DAMES CITY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Search completed: May 7 Job time: 13.7596 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94111-3834
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NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32,762
FRAGMENT TYPE: N-terminal ORIGINAL SOURCE: ORGANISM: Rana pipiens DEVELOPMENTAL STAGE: Occyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 13: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : 104 amino acids
amino acid
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                                                                                                                                             Best Local Similarity
Matches 54; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94111-3834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-891-848-13
                                                                     ;
US-08-467-955-1
                                                                                                                                Query Match
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                                                                                                                                                                                                                                       1 QNWATFQQKHIINT-PIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NMN
                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/08467955
Patent No. 5728805
Patent No. 5728805
GENERAL INFORMATION:
APPLICANT: Ardelt Ph.D, Wojciech J.
APPLICANT: ARACEL Ph.D, Wojciech J.
TITLE OF INVENTION: PHARMACEUTICALS AND METHOD FOR MAKING THEM NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mark H. Jay, P.A.
STREET: No. Box E
CITY: Short Hills
STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                 59 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
                                                                                                                                                                                            6
                                                                                                                                                      Length 104;
                                                                                                                                                  45.6%; Score 274.5; DB 1; Length 1 ilarity 48.6%; Pred. No. 1.7e-24; Conservative 16; Mismatches 32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PATENT: PC-LUOS, MS-LUOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,955
FILING DATE:
CLASSIFICATION NUMBER: US 07/178,118
FILING DATE: 06-APR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/436,141
FILING DATE: 06-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/436,141
FILING DATE: 03-FEB-1992
FILING DATE: 03-FEB-1992
FILING DATE: 01-AUG-1994
ATTORNEY/AGENT INFORMATION:
NUMBER: US 07/814,332
FILING DATE: 01-AUG-1994
ATTORNEY/AGENT INFORMATION:
NUMBER: US 07/814,332
FILING DATE: 01-AUG-1994
ATTORNEY/AGENT INFORMATION:
NUMBER: US 07/814,332
FILING DATE: 01-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 27507
REFERENCE/DOCKET NUMBER: 5007 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-912-9066
TELEFAX: 201-912-0442
TELEFAX: No. 5728805 Applicable
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
             FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Rana pipiens
DEVELOPMENTAL STAGE: Embryo
US-07-921-619-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 07078-0383
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 104 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein
                                                                                                                                  linear
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HYPOTHETICAL: N
    z
    ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 12
US-08-467-955-1
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1 EDWLIFQKKHITNTRDVDCDNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN 56
                                                                                                                     1 QNWATFOOKHIINT-PIICNTIMDNNIYIVGGOCKRVNTFIISSATTVKAICTGVI-NMN
                                                             Gaps
                                                                                                                                                                                                                                  59 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
                                                                                                                                                                                                                                                                  57 VLITSEFYLSDC---NVISRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 104
ch 45.6%; Score 274.5; DB 1; Length 104; I Similarity 48.6%; Pred. No. 1.7e-24; 54; Conservative 16; Mismatches 32; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Youle, Richard J.
APPLICANT: Youle, Richard J.
APPLICANT: Newton Dianne L.
APPLICANT: Nicholis, Peter J.
TITLE OF INVENTION: Selective RNase Cytotoxic Reagents
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FO Comparible
OPERATUR SYSTEM: FC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: NO. 5955073 yet assigned
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOUOXIC F. COUNTESSE:
LOUNESSE: Townsend and Crew LLP STREET: Two Binbarcadero Center, Eighth Floor STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        015280-110310US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/125,462
FILING DATE: 22-68F-1993
FILING DATE: 22-68F-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/014,082
FILING DATE: 04-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/779,195
FILING DATE: 22-OCT-1991
PRIOR APPLICATION NUMBER: US 07/510,696
FILING DATE: 20-DRP-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 13, Application US/08891848
Patent No. 5955073
GENERAL INFORMATION:
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Gaps

6

Length 104; Indels

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1 QNWATFQQKHIINT-PIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NMN 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Ardelt Ph.D, Wojciech J.
APPLICANT: Ardelt Ph.D, Wojciech J.
APPLICANT: Mikulski, Stanislaw M.
TITLE OF INVENTION: PHARMACEUTICAL FOR TREATING TUMORS IN HUMANS
TITLES OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mark H. Jay, P.C.
STREET: P.O. Box 020083, General Post Office
CITY: Brooklyn
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
45.6%; Score 274.5; DB 1;
Best Local Similarity 48.6%; Pred. No. 1.7e-24;
Matches 54; Conservative 16; Mismatches 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 19920728
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/178,118
FILING DATE: 06-APR-1988
PRIOR APPLICATION NUMBER: US 07/436,141
FILING DATE: 13-NOV-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/921,619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 11202-0002
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 718-625-0399
TELEX: No. 5595734 Applicable INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERESTICS: LENGTH: 104 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/07921619
Patent No. 5595734
                                                                                                                                                                                                                                                                                                ) ORGANISM: Rana pipiens
) DEVELOPMENTAL STAGE: Embryo
US-08-283-971-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Jay, Mark H.
REGISTRATION NUMBER: 27507
REFERENCE/DOCKET NUMBER: 501
TELECOMMUNICATION INFORMATION:
TELEPHONE: 718-625-0399
             104 amino acids
                                                                                                                                                                                                                                   FRAGMENT TYPE: N-terminal ORIGINAL SOURCE:
                                        TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                     MOLECULE TYPE: protein
HYPOTHETICAL: N
ANTI-SENSE: N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein HYPOTHETICAL: N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-07-921-619-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26 QDWLTFQKKHITNTRDVDCDNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ### Sequence 1, Application US/08283971

### Sequence 1, Application US/08283971

### Patent No. 5529775

### GENERAL INFORMATION:

### APPLICANT: Ardelt Ph.D, Wojciech J.

### APPLICANT: Ardelt Ph.D, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 379;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
46.1%; Score 277.5; DB 3; Length
Best Local Similarity 49.5%; Pred. No. 3.7e-24;
Matches 55; Conservative 15; Mismatches 32; Indels
             FILING DATE: 21-FBB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Faris, Susan K.
RECISTRATION NUMBER: 41,739
RECISTRATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECHOME: (415) 576-0300
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 379 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRICE APPLICATION 1933.

APPLICATION NUMBER: US 07/921,180 FILING DATE: 30-UUL-1992 APPLICATION NUMBER: US 07/178,118 FILING DATE: 06-APR-1988 PRIOR APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: US 07/436,141 FILING DATE: 13-NOV-1989 ATTORNEY/AGENT INFORMATION:
US 60/011,800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/283,971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5006 US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Jay, Mark H.
REGISTRATION NUMBER: 27507
REFERENCE/DOCKET NUMBER: 50.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 718-625-0399
                                                                                                                                                                                                                                                                                                                                                  : 379 amino acids
amino acid
3Y: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               718-625-0399
                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
CLASSIFICATION: 435
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-875-811-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 10
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MEDIUM TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         qq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Boix, Ester APPLICANT: Boix, Ester APPLICANT: Ardelt, Wojeiech APPLICANT: Ardelt, Wojeiech TITLE OF INVENTION: Allows Production by Recombinant Methods NUMBER OF SEQUENCES: 3
CORRESPONDENES: ADDRESS: ADDRESSE: Townsend and Townsend and Crew STREET: One Market Plaza, Steuart Street Tower CITY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    46.1%; Score 277.5; DB 4; Length 104; 49.5%; Pred. No. 7.7e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 63, Application US/08875811
| Patent No. 6045793
| GENERAL INFORMATION:
| APPLICANT: ROWACO, Diame L. APPLICANT: Nowton, Diame L. APPLICANT: Nowton, Diame L. APPLICANT: Hoque, Lluis
| APPLICANT: Hodawer, Alexander TITLE OF INVENTION: Recombinant Ribonuclease Proteins (ORRESPONDENCE ADDRESS: 64)
| CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSEE: Two Embarcadero Center, Eighth Floor CITY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/095,429
FILING DATE:
CLASSIFICATION:
APPLICATION NUMBER: 08/626,288
FILING DATE:
APPLICATION NUMBER: 08/626,288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 15280-267
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEPAX: (415) 543-5043
INFORMATION POR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                ZIP: 94105-1492
COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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NAME: Ran, David B.
REGISTRATION NUMBER: 38,589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 104 amino acids TYPE: amino acid
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  Wu, Yon-Neng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
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COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                  USA
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US-08-875-811-63
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  APPLICANT:
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1 QNWATFQOKHIINT-PIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NNN 58
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; Sequence 43, Application US/08875811
; Patent No. 6045793
; GENERAL INFORMATION:
    APPLICANT: Rybak, Susamna M.
    APPLICANT: Newton, Dianne L.
    APPLICANT: Newton, Dianne L.
    APPLICANT: Rlodawer, Alexander
    TITLE OF INVENTION: Recombinant Ribonuclease Proteins
    NUMBER OF SEQUENCES: 64
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
46.1%; Score 277.5; DB 3; Length:
Best Local Similarity 49.5%; Pred. No. 1e-24;
Matches 55; Conservative 15; Mismatches 32; Indels
                                                                  OFFRAINGS SYSTEM:
CURRENT APPLICATION DATA:
SOFTWARE PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
CLASSIFICATION 1435
PRIOR APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION NUMBER: WS 60/011,800
FILING DATE: 21-FEB-1996
ATTONEY/AGENT INFORMATION:
NAME: RATIS, SUBBAR: 41,739
REGISTRATION NUMBER: 41,739
RELECOMMUNICATION INFORMATION:
TELECHOME. (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PatentIn Release #1.0, Version #1.30
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Two Embarcadero Center, Bighth Floor
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APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
CLASSIFICATION: 435
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (415) 576-0300 INFORMATION FOR SEQ ID NO: 6 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : 129 amino acids
amino acid
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CITY: San Francisco
STATE: California
COUNTRY: USA
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Matches

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1 ONWATFOOKHIINT-PIICNTIMDNNIYIVGGOCKRVNTFIISSATTVKAICTGVI-NMN
                                                                59 VLSTTRFQLNTCTRISITPRPCPYSSRTEINYICVKCENQYPVHFAGIGRC 109
                                                                                         59 VLSTTREQLNTCTRISITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Wu, You-not APPLICANT: Wu, You-not APPLICANT: Boix, Ester APPLICANT: Adelt, Wolsen APPLICANT: Adelt, Wolsen Form of Cytotoxic Protein Which TITLE OF INVENTION: Allows Production by Recombinant Methods NUMBER OF SEQUENCES: ADRESSEE: Townsend and Townsend and Crew STRET: One Market Plaza, Steuart Street Tower CITY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPOTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/626,288
FILING DATE: No. 6649392 yet assigned
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 4;
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llarity 49.5%; Pred. No. 7.7e-25;
Conservative 15; Mismatches 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Ran, David B.
REGISTATION NUMBER: 38,589
REFRENCE/DOCKET NUMBER: 15280-267
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
                                                                                                                                                                                                    ; Sequence 1, Application US/08626288
; Patent No. 6649392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/09095429
; Patent No. 6649393
; GENERAL INFORMATION:
    APPLICANT: Youle, Richard
                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Youle, Richard
APPLICANT: Vasandani, Veena
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Youle, Richard APPLICANT: Vasandani, Veena
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Sar
STATE: Ca
COUNTRY:
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US-08-626-288-1
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US-09-095-429-1
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Best Local
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APPLICANT: Saxena, Shailendra K
TITLE OF INVENTION:
METHODS OF MAKING NUCLEIC ACIDS ENCODING RIBONUCLEASES
FILE REPRENCE: 5013 US 019/687,748
CURRENT APPLICATION NUMBER: US/09/687,748
PRIOR PILING DATE: 1200-10-14
PRIOR FILING DATE: 1999-09-10
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PALENTIN VET: 2.0
                                                                                                                                 1 ONWATFOCKHIINT-PIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NMN 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ONWATFQQKHIINT-PIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NMN 58
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                                                                                                                                                                    1 EDWLTFOKKHVINTRDVDCNNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN
                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/09394268
Patent No. 6475003
GENERAL INFORMATION:
APPLICANT: Saxena, Shailendra K
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING RIBONUCLEASES AND METHODS OF
TITLE OF INVENTION: MAKING THEM
                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                            59 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENOYPVHFAGIGRC 109
                                                                                                                                                                                                                                   VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
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                                                              Length 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  46.1%; Score 277.5; DB 3; Length 104; 49.5%; Pred. No. 7.7e-25; Live 15; Mismatches 32; Indels 9
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                                                                                                 31, Indels
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                                                            DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32;
                                                        Score 284.5; DB 1 Pred. No. 1.2e-25;
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                                                                                               16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/394,268
CURRENT FILING DATE: 1999-09-10
NUMBER OF SEQ ID NOS: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/09687748 Patent No. 6423515
Oocyte
                                                        47.3%;
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                                                                                             55; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           55; Conservative
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DEVELOPMENTAL STAGE:
                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Rana pipiens
US-09-394-268-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Rana pipiens
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Best Local Similarity
Matches 55; Conserv
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Best Local Similarity
Matches 55; Conserv
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US-08-467-955-2
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Length 104;

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; OTHER INFORMATION: /note= "Frog Lectin from Rana ; OTHER INFORMATION: catesbeiana" US-08-875-811-8
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TELEX: No. 5728805 Applicable
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                               US-08-467-955-2
; Sequence 2, Application US/08467955
; Patent No. 5728805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 27507
REFERENCE/DOCKET NUMBER: 50
TELECOMMUNICATION INFORMATION:
                                                                                         Query Match 97.8%;
Best Local Similarity 98.2%;
Matches 109; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: 201-912-9066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 104 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein HYPOTHETICAL: N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Jay, Mark H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: New Je
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE
                                                                                                                                                                                                                            Dp
                                                                                                                                                                                                                                                                       \delta
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                                                                                                                                                                                                                                                                                                                                               1 QNWAIFQQKHIINTPII-CNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNV 59
                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                          60 LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
                                                                                                                                                                                                                                                                            1;
                                                                                                                                                                                                                            97.8%; Score 588.5; DB 2; Length 111; 98.2%; Pred. No. 7.4e-61; tive 1; Mismatches 0; Indels 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: Newton, Liuis
APPLICANT: Wiodawer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: Eloppy disk
COMPUTER: EN FC COMPATIBLE
COMPUTER: Floppy disk
CORERAING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
CLASSIFICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Faris, SUSAN K.
REGISTRATION NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 015280-244100US
TELLECOMMUNICATION NUMBER: 015280-244100US
                                                                                                                                  /note= "Frog Lectin from Rana
catesbelana"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco COUNTE: California COUNTEY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 8, Application US/08875811; Patent No. 6045793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEO ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 111 amino acids TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                              Query Match
Best Local Similarity 98.2<sup>3</sup>
Matches 109; Conservative
                                         MOLECULE TYPE: protein FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
                                                                                                                     COCATION: 1..111
CTHER INFORMATION:
COTHER INFORMATION:
US-08-891-848-12
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                                                                                                NAME/KEY: Protein
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                                    linear
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ZIP: 94111-3834
             STRANDEDNESS:
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1 QNWATFQQKHIINTPII-CNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNV 59
                                                                                                                                                1 ENWATFQQKHINTPINCNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMVV 60
                                                             1; Gaps
                                                                                                                                                                                                                               60 LSTTRFQLNTCTRISITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
                                                                                                                                                                                                                                                                61 LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCF 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Ardelt Ph.D, Wojciech J.
APPLICANT: Ardelt Ph.D, Wojciech J.
APPLICANT: Ardelt Ph.D, Wojciech J.
APPLICANT: Ardelt Ph.D, Wojciech J.
CORRESPONDENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mark H. Jay, P.A.
STREET: P.O. Box E
CITY: Short Hills
STAIE: New Jersey
Score 588.5; DB 3; Length 111;
Pred. No. 7.4e-61;
1; Mismatches 0; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/178,118
FILING DATE: 06-APR-1988
FRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/436,141
FILING DATE: 13-NOV-1989
FRIOR APPLICATION NUMBER: US 07/814,332
FILING DATE: 03-FEB-1992
FRIOR APPLICATION NUMBER: US 07/814,332
FRIOR APPLICATION NUMBER: US 08/283,970
FILING DATE: 01-AUG-1994
FILING DATE: 01-AUG-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Pacentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ANTI-SENSE: N
FRAGMENT TYPE: NORIGINAL SOURCE:
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ORGANISM: Rana pipiens

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7, 2004, 21:28:45 ; Search time 12.7596 Seconds (without alignments) 445.066 Million cell updates/sec
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1 QNWATFQQKHIINTPIICNT.....ICVKCENQYPVHFAGIGRCP 110
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1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                              389414 segs, 51625971 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                            OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                           Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                 Scoring table:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Sequence 12. Appl	i co	2	` -	ì ,-	Sequence 1, Appli	Ή.	9	4	Ì ,:	equence 1.	ì		30	7 1	Segmence 51 Appl		Sequence 2. Appli		'n	ì	28.	2	2 6	o u	, ,	
SUMMARIES	US-08-891-848-12	US-08-875-811-8	US-08-467-955-2	-09-394-	-681-	-08-626-28	US-09-095-429-1	US-08-875-811-63	US-08-875-811-43	US-08-283-971-1	-921-619-	-955	US-08-891-848-13	US-08-875-811-39		-08-875-811	-875-811-	US-09-394-268-2	US-09-071-672-1	US-09-687-748-2	-09-98	US-08-875-811-28	US-08-875-811-30	-811-3	-08-875-811-	-875-811-6	-08-875-811-
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Length	111	111	104	104	104	104	104	129	379	104	104	104	104	105	355	358	104	104	104	104	104	106	107	112	251	254	355
% Query Match	97.8	97.8	47.3	46.1	46.1	٠	46.1	٠				•				45.6		ŝ	٠	•	45.3		45.3	45.3	45.3	45.3	45.3
Score		588.5		277.5	77.	•	•	•	277.5							274.5			•	72.	272.5		272.5			272.5	72.
Result No.	Н	7	٣	4	IJ	9	7	8	6	10	11	12	13	14	15	16	17	H 8	19	20	21	22	23	24	25	26	27

Sequence 57, Appl	Sequence 64, Appl	55.	2. A	2	24	26.	45	53	20.	22		47	2	ı .	4	S	'n
US-08-875-811-57	US-08-875-811-64	US-08-875-811-55	US-08-626-288-2	US-09-095-429-2	US-08-875-811-24	US-08-875-811-26	US-08-875-811-45	US-08-875-811-53	US-08-875-811-20	US-08-875-811-22	US-09-223-118-3	US-08-875-811-47	US-09-223-118-2	US-09-223-118-1	US-09-223-118-4	US-08-875-811-2	US-09-071-672-3
355 3	355 3	366 3	104 4	104 4	105 3	.05 3	158 3	165 3	.07 3	111 3	114 3	60 3	14 3	.14 3	114 3	83 3	83 4
5 45.3	5 45.3	272.5 45.3 3	269.5 44.8 1	269.5 44.8 1	5 44.4	5 44.4		43.8	249.5 41.4 1		236 39.2 1				37.4	206 34.2	
28	5.5	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

	ZIP: 94111-3884 COMPUTER READBLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DoS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/91,848 FILING DATE: No. 5955073 Yet assigned CLASSIFICATION NUMBER: US/08/125,462 FILING DATE: 22-SEP-1993 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/125,462 FILING DATE: 22-CST-1993 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/014,082 FILING DATE: 22-CCT-1991 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 07/779,195 FILING DATE: 20-ARE-1990 ATTORNEY/AGENT INFORMATION: RECISTRATION NUMBER: US 07/510,696 FILING DATE: 20-ARE-1990 ATTORNEY/AGENT INFORMATION: RECISTRATION NUMBER: US 07/510,696 FILING DATE: 20-ARE-1990 ATTORNEY/AGENT INFORMATION: RECISTRATION NUMBER: US 07/510,696 TELECOMMUNICATION INFORMATION: TELEFAX: (415) 576-0300 INFORMATION FOR SEQ ID NO: 12: SEQUENCE CHARACTERISTICS: LENGTH: LIL mainto acide TTPE: amino acide
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a synthetic ribonuclease protein, in

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Amino acid sequence of a frog ribonuclease protein.
                                                                                                                                                                                                                                                          Frog; ribonuclease; ranpirnase; RNase
                                                                                                                                                                                                                     AAB31666 standard; protein; 104 AA
                                                                                                                                                                                                                                                                                                                  99US-00394268.
                                                                                                                                                                                                                                                                                                                            99US-00394268
                                                                                                                                                                                                                                        30-APR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                     (ALFA-) ALFACELL CORP
                                                                                                                                      Sequence 104 AA;
                                                                                                                                                                                                                                                                              Key
Modified-site
Rana pipiens
         WO9738112-A1
                            04-APR-1997;
                                     04-APR-1996;
                                                                                                                                                                                                                                                                    Rana pipiens
                                                                                                                                                                                                                                                                                                US6175003-B1
                                                                                                                                                                                                                                                                                                                  10-SEP-1999;
                                                                                                                                                                                                                                                                                                                            10-SEP-1999;
                                                                                                                                                                                                                                                                                                         16-JAN-2001.
                   16-0CT-1997
                                                        Youle RJ,
                                                                                                                                                                                                                                                                                                                                               Saxena SK;
                                                                                                                                                                                             57
                                                                                                                                                                                                                               AAB31666
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/note= "this Gln is autocyclised to pyroglutamic acid"

Location/Qualifiers

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New nucleic acids encoding a ribonuclease (Rnase), useful for the precise targeting of Rnase to a predetermined cell receptor.
                                                                                                                                                                                          The present sequence represents a frog ribonuclease protein (ranpirnase) (RNase). The specification describes a synthetic ribonuclease protein, in which the addition of cysteine in the ribonuclease facilitates the chemical linking of a targeting molecule by the single reactive sulfhydryl group. The specification also describes a method for the production of ranpirnase using DNA technology instead of processing biological material. The re-engineering of the protein molecule allows easier attachment to a targeting molecule thereby making it possible for the ribonuclease to be delivered to a particular cell receptor where it might be most effective
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Search completed: May 7, 2004, 21:38:28
Job time : 46.9224 secs
                                                                                                                                                Claim 1; Col 5-6; 7pp; English.
                     WPI; 2001-167808/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence represents a recombinant Onc protein comprising a 104 amino acid sequence having Gln at position 1. Onc, a ribonuclease from Rana pipiens occytes, is known as an antitumour agent (e.g. for treating pancreatic cancer) and inhibitor of human immunodeficiency virus type-1 replication. It can be used therapeutically or as a cell-culture selection agent, e.g. to identify gene therapy compositions able to inhibit tumour growth
                                                                                                                                                                                                                                                                                                                                                                                                     Recombinant Onc protein with glutamine residue at position 1 - useful as antitumour and antiviral agent, also as cell culture selection agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ODWLIFOKKHIINTRDVDCDNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VLTTSEFYLSDC---NVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 104;
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                                                                                                                                                                                                                                                                                                     Ardelt W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Score 277.5; DB 2;
; Pred. No. 8.3e-24;
15; Mismatches 32;
                                                                                                                                                                                                                                                                                                     Boix E,
                                                                                                                                                                                                                                                (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                     Wu Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 28; 35pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           46.18;
                                                                                                                                                97WO-US005675.
                                                                                                                                                                                                  96US-00626288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 49.5'
Matches 55; Conservative
                                                                                                                                                                                                                                                                                                     Vasandani VM,
                                                                                                                                                                                                                                                                                                                                                        WPI; 1997-512725/47.
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                                                                                                         1 QNWATFQQKHIINT-PIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NMN
                                                           Gaps
                                                                                                                                                 59 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
                                                                                                                                                                     6
                            DB 4; Length 104;
                                                         Indels
                           46.1%; Score 277.5; DB 4 49.5%; Pred. No. 8.3e-24; iive 15; Mismatches 32
                                                           Conservative
                                         Similarity
Sequence 104 AA;
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us-09-961-400-15.rag

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The present sequence is a recombinant Rana pipiens ribonuclease (RaPLR1) protein with Met23Leu. Carboxy terminal end of recombinant RaPLR1 has a dovalently bound ligand binding moiety, which can be a LL2 antibody directed against CD22 on cancerous B cells or human chorionic gonadotrophin (hCG) effective against Kaposi's sarcoma cells. Recombinant ribonucleases can be expressed in bacteria without an N-terminal methionine due to the presence of a signal peptide that is cleaved by bacteria. The soluble expression of ribonuclease allows the proteins to be fused in-frame with ligand binding moieties to form cytocoxic fusion proteins. They can be used for treatment of cancer and autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Recombinant Met(-1) Rana pipiens ribonuclease Met23Leu-(His)6; RaPLR1; CD22; covalently bound; LL2 antibody; ligand binding moiety; RNase; cancerous B cell; Kaposi's sarcoma; human chorionic gonadotrophin; hCG; signal peptide; recombinant ribonuclease; cytotoxic fusion protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                             New recombinant ribonucleases, used for killing target cells, e.g. for treating cancers, viral infections or autoimmune diseases.
LL2 antibody; ligand binding moiety; CD22; cancerous B cell; RNase; Kaposi's sarcoma; human chorionic gonadotrophin; hCG; signal peptide; recombinant ribonuclease; cytotoxic fusion protein; cancer; frog;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 QNWATFQQKHIINT-PIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NMN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QDWLTFQKKHLTNTRDVDCNNILSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                   /note= "Wild type Met replaced with Leu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Recombinant Met(-1) RaPLR1 Met23Leu-(His)6 protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 278.5; DB 2;
Pred. No. 6.4e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16; Mismatches
                                                                                                                                                                                                                                                                                                                                (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 34; Page 56; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY28869 standard; protein; 105
                                                                                                                                                                                                                                                                  99WO-US006641.
                                                                                                                                                                                                                                                                                                   98US-0079751P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              46.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54; Conservative
                                                                                                                                                                                                                                                                                                                                                                Rybak SM, Newton DL;
                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1999-610847/52.
                                                      autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAZ08125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 104 AA;
                                                                                                                                                  Misc-difference
                                                                                      Rana pipiens
                                                                                                                                                                                                                                                                 26-MAR-1999;
                                                                                                                                                                                                                                                                                                   27-MAR-1998;
                                                                                                                                                                                                  WO9950398-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-JAN-2000
                                                                                                                                                                                                                                07-0CT-1999
                                                                                                      Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY28869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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The present sequence is a recombinant Rana pipiens ribonuclease protein (RaPLR1) with Met at position 1 attached to (His)6 tag and Met24Leu. Carboxy terminal end of recombinant RaPLR1 has a covalently bound ligand binding moiety, which can be a LL2 antibody directed against CD22 on cancerous B cells or human chorionic gonadotrophin (hCG) effective against Kaposi's sarcoma cells. Recombinant ribonucleases can be expressed in bacteria without an N-terminal methionine due to the presence of a signal peptide that is cleaved by bacteria. The soluble expression of ribonuclease allows the proteins to be fused in-frame with ligand binding moieties form expression proteins. They can be need for treatment of cancer and authorizants.
                                                                                                                                          note= "(His)6 histidine tag attached to N-terminal Met"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 ODWITFOKKHITNTRDVDCNNILSTNIF --- HCKDKNTFIYSRPEPVKAICKGIIASKN 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                           New recombinant ribonucleases, used for killing target cells, e.g. for treating cancers, viral infections or autoimmune diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 QNWATFQQKHIINT-PIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NMN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Onc; oncanase; ribonuclease; frog; antitumour; pancreatic cancer; human immunodeficiency virus type-1; HIV1; replication.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENOYPVHFAGIGRC 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VLTTSEFYLSDC---NVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .;6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 105;
                                                                                                               'note= "Met not found in wild type RaPLR1'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                             /note= "Wild type Met replaced with Leu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             used for treatment of cancer and autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           46.3%; Score 278.5; DB 2
48.6%; Pred. No. 6.5e-24;
iive 16; Mismatches 32
                                                                                                                                                                                                                                                                                                                                            (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW30301 standard; protein; 104 AA.
cancer; frog; autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 4; Page 59; 71pp; English
                                                                                                                                                                                                                                                                                99WO-US006641.
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                                                                                                                                                                                                                                                                                                                                                                              Newton DL;
                                                                                                                                                                                                                                                                                                                                                                                                           WFI; 1999-610847/52.
N-PSDB; AAZ08127.
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                                                                                                                              Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 105 AA;
                                                                                              Misc-difference
                                                                                                                                                               Misc-difference
                             Rana pipiens.
Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                            Rybak SM,
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Kaposi's Sarcoma, human chorionic gonadotrophin; hCG; cancer; recombinant ribonuclease; frog; signal peptide; cytotoxic fusion protein;

autoimmune disease.

Rana pipiens

Peptide

Protein

24. .127 /label= Rana_pipiens_Clone_5alb_ribonuclease

1. .23 /label= Signal_peptide /note= "Putative" Location/Qualifiers

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Rana pipiens Clone 5alb ribonuclease.
                                                                                                                                                                                    AAY28879 standard; protein; 127 AA
                                                                                                                                                                                                (first entry)
                    Rana pipiens.
Synthetic.
                                                   26-MAR-1999;
                                                                                                                                                                                                25~JAN-2000
                                                         27-MAR-1998;
                                       WO9950398-A2
                                             07-0CT-1999
                                                                                                                                               55;
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                                                                                                                                                                                          AAY28879;
                                                                                                                                         Query Match
                                                                    Rybak
                                                                                                                                               Matches
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Recombinant Met(-1) Rana pipiens ribonuclease; RaPLR1; CD22; RNase; covalently bound; LL2 antibody; ligand binding moiety; cancerous B cell; Raposi's sarcoma; human chorionic gonadotrophin; hCG; signal peptide; recombinant ribonuclease; cytotoxic fusion protein; cancer; frog; autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New recombinant ribonucleases, used for killing target cells, e.g. treating cancers, viral infections or autoimmune diseases.
                                                                                                                                                                                                                                                                                                                                                                                                  /note= "Met not found in wild type RaPLR1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (USSH ) US DEPT HEALTH & HUMAN SERVICES
                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 34; Page 57; 71pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99WO-US006641.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1999-610847/52.
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                                                                                                                                                                                                                                                                                                                                                              Misc-difference
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gonadotrophin (hCG) effective against Kaposi's sarcoma cells. Recombinant ribonucleases can be expressed in bacteria without an N-terminal methicnine due to the presence of a signal peptide that is cleaved by bacteria. The soluble expression of ribonuclease allows the proteins to be fused in-frame with ligand binding moieties to form cytotoxic fusion proteins. They can be used for treatment of cancer and autoimmune diseases 28 57 The present sequence is a recombinant Rana pipiens ribonuclease (RaPLR1) protein with Met at position 1. Carboxy terminal end of recombinant RaPLR1 has a covalently bound ligand binding moiety, which can be a LL2 antibody directed against CD22 on cancerous B cells or human chorionic ODWLTFOKKHLINTRDVDCNNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN 1 QNWATFQQKHIINT-PIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NWN Gaps VLSTTRFQLNTCTRISITPRPCPYSSRTEINYICVKCENQYPVHFAGIGRC 109 6 DB 2; Length 105; Indels 32; Score 281.5; DB 2 Pred. No. 2.9e-24; 5; Mismatches 32 15; 46.8%; Conservative Local Similarity

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Recombinant Rana pipiens ribonuclease; RaPLR1 Met23Leu; covalently bound;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ONWAIFQOKHIINT-PIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NMN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24 ODWLTFOKKHLTNTRDVDCNNIMSTNLF---HCKDKNTFIYSRPEPVKAICKGIIASKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VLTTSEFYLSDC---NVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Recombinant RaPLR1 Met23Leu amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 46.8%; Score 281.5; DB 2
49.5%; Pred. No. 3.7e-24;
cive 15; Mismatches 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY28866 standard; protein; 104 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 127 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-JAN-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rana pipiens ribonuclease Clone 5alb; RaPLR1; covalently bound; RNase; LL2 antibody; ligand binding moiety; CD22; cancerous B cell; onconase;
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4,

The present sequence is a Rana pipiens clone 5alb ribonuclease (RaPLRI). It is encoded by Clone 5alb cDNA obtained from Rana pipiens liver mRNA library. It exhibits differences with Oncoase (RTM) at amino acid residues 11, 20, 85 and 103. Carboxy terminal end of RaPLRI has a covalently bound ligand binding moiety, which can be a LL2 antibody directed against CD22 on cancerous B cells or human chorionic gonadotrophin (hCG) effective against Kaposi's Sarcoma cells. Recombinant ribonucleases can be expressed in bacteria without an N-terminal methicnine due to the presence of a signal peptide that is cleaved by bacteria. The soluble expression of ribonucleases allows the proteins to be fused in-frame with ligand binding moieties to form cytotoxic fusion proteins. They can be used for treatment of cancer and autoimmune

New recombinant ribonucleases, used for killing target cells, e.g. for treating cancers, viral infections or autoimmune diseases.

Disclosure; Page 69; 71pp; English.

(USSH) US DEPT HEALTH & HUMAN SERVICES.

Newton DL;

Rybak SM,

1999-610847/52.

N-PSDB; AAZ08136

for

99WO-US006641. 98US-0079751P

26-MAR-1999; 27-MAR-1998;

WO9950398-A2

07-0CT-1999

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SXS

RESULT 8 AAW06544

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The present sequence is Rana pipiens liver ribonuclease (RaPLR1) protein. Carboxy terminal end of RaPLR1 has a covalently bound ligand binding moiety, which can be a LL2 antibody directed against CD22 on cancerous B cells or human chorionic gonadotrophin. (hCG) effective against Kaposi's Sarcoma cells. Recombinant ribonucleases can be expressed in bacteria without an N-terminal methionine due to the presence of a signal peptide that is cleaved by bacteria. The soluble expression of ribonuclease allows the proteins to be fused in-frame with ligand binding moieties to form cytotoxic fusion proteins. They can be used for treatment of cancer and autoimmune diseases
                                                                                                                                                                                                      Rana pipiens liver ribonuclease, RaPLR1; covalently bound; LL2 antibody, ligand binding moiety; CTD2; cancerous B cell; Kaposi's Sarcoma; frog; human chorionic gonadotrophin; hCG; recombinant ribonuclease; RNase; signal peptide; cytotoxic fusion protein; cancer; autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ONWATFQOKHIINT-PIICNTIMDNNIYIVGGOCKRVNTFIISSATTVKAICTGVI-NMN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New recombinant ribonucleases, used for killing target cells, e.g. treating cancers, viral infections or autoimmune diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENOYPVHFAGIGRC 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         46.8%; Score 281.5; DB 2
49.5%; Pred. No. 2.9e-24;
ive 15; Mismatches 32
                                                                                                                                                                    Rana pipiens liver ribonuclease (RaPLR1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                            AAY28865 standard; protein; 104 AA.
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                                                                                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Newton DL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1999-610847/52.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAZ08124
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                                                                                                                                                                                                                                                                                                 Rana pipiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SM,
                                                                                              AAY28865;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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Matches
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                                           AAY28865
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                                                                                                                 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence is a specifically claimed example of an antitumour protein from the generic protein in AAW18224, with the molecular weight 12000. This is one of two preferred proteins (the other in AAW6543) that have been isolated from Rana pipiens occytes. Both proteins have a blocked amino terminal group and are essentially free of carbohydrates. The proteins are used to treat tumours. Use of the peptides has fewer disadvantages than chemotherapy, radiotherapy and surgery in the treatment of tumours
                                                                                                                                                   29
                                                                                                                                                                      ENWAIFQQKHIINTPIINCNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26
(Rana catesbelana) lectin used to describe the method of the invention
                                                                                                                                               1 QNWATFQQKHIINTPII-CNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ONWATEOOKHIINT-PIICNTIMDNNIYIVGGCCKRVNTFIISSATTVKAICTGVI-NMN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EDWIJFOKKHVINIRDVDCNNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIJASKN
                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                    LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VLSTTRFQLNTCTRISITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 104;
                                                                           Length 111;
                                                                                                                                                                                                                                                LSTIREQLNICIRISITERECPYSSRIEINVICVKCENQYPVHFAGIGRCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antitumour proteins from Rana pipiens oocyte(s) - have fewer disadvantages than chemotherapy, surgery and radiotherapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                               Indels
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                                                                           DB 2;
                                                                       Score 588.5; DB 2
Pred. No. 2.2e-59;
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; Pred. No. 1.3e-24;
16; Mismatches 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antitumour protein from Rana pipiens oocytes.
                                                                                                             1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tumour; chemotherapy; radiotherapy; frog.
                                                                                                                                                                                                                                                                                                                                                AAW06544 standard; protein; 104 AA
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                                                                      97.8%;
98.2%;
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                                                                                                           Conservative
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                                                                                          Similarity
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                                     Sequence 111 AA;
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Best Local Simil
Matches 55; C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rana pipiens.
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                                                                                          Sest Local Sim
Matches 109;
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Length 104; Indels

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99.0%; Score 596; DB 2; 98.2%; Pred. No. 3e-60; ive 2; Mismatches

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Length 111; Indels 9

ONWALFOOKHIINTPIICNTIMDNNIYIVGGOCKRVNTFIISSATTVKAICTGVINMNVL

(USSH) US DEPT HEALTH & HUMAN SERVICES Location/Qualifiers Claim 22; Page 66; 71pp; English. AAY28876 standard; protein; 111 99WO-US006641. 98US-0079751F. Rybak SM, Newton DL; WPI; 1999-610847/52. catesbeiana N-PSDB; AAZ08133 Misc-difference Misc-difference Misc-difference Misc-difference 27-MAR-1998; WO9950398-A2 25-JAN-2000 07-0CT-1999 Synthetic AAY28876; Н 61 Rana RESULT 6 AAY28876 g Š

The present sequence is a recombinant Rana catesbelana oocyte ribonuclease (RaCOR1) protein with Met at position 1 attached to a (His)6 tag, Met21Jeu and Met58Leu. Carboxy terminal end of recombinant RaCOR1 has a covalently bound ligand binding moiety, which can be a LL2 antibody directed against CD22 on cancerous B cells or human chorionic gonadotrophin (hCG) effective against Kaposi's sarcoma cells. Recombinant ribonucleases can be expressed in bacteria without an N-terminal methionine due to the presence of a signal peptide that is cleaved by bacteria. The soluble expression of ribonuclease allows the proteins to be fused in-frame with ligand binding moieties to form cytotoxic fusion proteins. They can be used for treatment of cancer and autoimmune Sequence 111 AA;

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Met (-1) Rana catesbeiana ribonuclease Met22Leu Met57Leu-(His)6; RaCOR1; recombinant; CD22; covalently bound; LL2 antibody; ligand binding moiety; cancerous B cell; Kaposi's sarcoma; human chorionic gonadotrophin; hCG; signal peptide; recombinant ribonuclease; cytotoxic fusion protein; cancer; bullfrog; RNase; autoimmune disease.
                                          note= "(His)6 histidine tag attached to N-terminal Met"
ONWATFQOKHIINTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNVL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New recombinant ribonucleases, used for killing target cells, e.g. treating cancers, viral infections or autoimmune diseases.
                                                                                                                                                                            110
                                                                                                                                                                                                                                                                 STIRFQLNICIRISITPRPCPYSSRIEINYICVKCENQYPVHFAGIGRCP 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Recombinant Met(-1) RaCOR1 Met22Leu Met57Leu-(His)6 protein.
                                                                                                                                                                            STTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENOYPVHFAGIGRCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note= "Met not found in wild type RaCOR1"
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in immune and autoimmune diseases. Additionally, they may be used as contraceptives. Finally they can also be used for cell separation in vitro by selectively killing unwanted types of cells (e.g. in bone marrow) prior to transplantation into a patient undergoing marrow ablation by radiation or for killing leakemia cells or T-cells that would cause graft-versus-host disease. This sequence represents a bullfrog This invention describes a novel nucleic acid construct comprising sequences encoding functional pancreatic RNase and a second protein (preferably the light and heavy chains of an antibody) which binds a specific cell surface marker on a target cell and functions as a cytotoxic agent. The products can be used for selectively killing cells tumors or infected cells (e.g. cells infected by viruses (sepecially latent or chronic virus infections, such as human immunodeficiency virus (HIV)-1, Epstein-Barr virus, herpes viruses (herpes simplex types I and II), hepatitis viruses (8, non-A-non-B, and delta), herpes zoster, cytomegalovirus)) and cells infected with parasites (such as the malaria parasite)). They can also be used for treating immune dysfunctional cells 2 QNWATFQQKHIINTFIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINLNVL 61 heavy chain; cell surface marker; treatment; tumor; viral infection; parasite infection; immune dysfunctional cell; autoimmune disease; contraceptive; cell separation; transplantation; bone marrow ablation; leukemia cell; T-cell; graft-versus-host disease; bullfrog; lectin. nntly fused pancreatic RNase-targeting proteins useful for tumors, infections, immune or autoimmune disorders and as Cytotoxic; RNase; ribonuclease; pancreatic; antibody; light chain; STTRFQLNTCTRISITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110 STIRFQLNICTRISITERPCPYSSRTEINVICVKCENQYPVHFAGIGRCP 111 Nicholls PJ, Youle RJ; (USSH) US DEPT HEALTH & HUMAN SERVICES. Ā Example 3; Fig 19; 47pp; English. AAY33321 standard; protein; 111 90US-00510696. 91US-00779195. 93US-00014082. 93US-00125462. fragment. 97US-00891848. (first entry) Newton DL, Frog lectin protein WPI; 1999-560488/47 Recombinantly fused catesbeiana. contraceptive. 29~NOV-1999 , 79e1-JUL-60 20-APR-1990; 22-OCT-1991; 22-SEP-1993; 04-FEB-1993; US5955073-A. 21-SEP-1999 Rybak SM, AAY33321; treating 61 Rana AAY33321 RESULT g à

Indels

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                                                                                                                                                                                                                                                                                                                                                                  Recombinant Met (-1) Rana catesbeiana occyte ribonuclease Gln1Ser; RacOR1, coadaently bound. LL2 antibody, ligand binding moiety; cancerous B cell; Kaposi, s sarcona; human chorionic gonadotrophin; hCG; signal peptide; recombinant ribonuclease; cytotoxic fusion protein; cancer; bullfrog;
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                                                                                     NWATFQQKHIINTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMVVLS
                                                            NWATFQQKHIINTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNVLS
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                                                                                                                          TTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP
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                               Indels
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           . 2.3e-60;
ches 0;
                              Mismatches
             Pred. No.
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100.0%; Pr.
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                            109; Conservative
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           Best Local Similarity
Matches 109; Conser
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Length 111;

99.2%; Score 597; DB 2; I 100.0%; Pred. No. 2.3e-60;

Query Match Best Local Similarity

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                                                            62
                                 61
                                                                                                                                                                                                                                                                                                                                    Recombinant Rana catesbeiana oocyte ribonuclease; covalently bound; RaCORI Met22Leu Met57Leu; LLZ antibody; ligand binding moiety; CD22; cancerous B cell; Kaposi's sarcoma; human chorionic gonadotrophin; hCG; signal peptide; recombinant ribonuclease; cytotoxic fusion protein; cancer; bullfrog; RNase; autoimmune disease.
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                                                     3 NWAIFQQKHIINTPIICNTIMDNNIYIVGGQCKRVNIFIISSATTVKAICTGVINMVVLS
                              2 NWAIFQQKHIINTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNVLS
   Gaps
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                                                                                                                TTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
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                                                                                                                                                                                                                                                                                                      Recombinant RaCOR1 Met22Leu Met57Leu amino acid sequence.
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Pred. No. 3e-60;
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0; Mismatches
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Matches 108, Conservative
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Length 111;

Score 602; DB 2; Pred. No. 6.2e-61;

100.0%;

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                                                                   Matches 110; Conservative
                                                   Similarity
   Sequence 111 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Recombinant Met(-1) Rana catesbeiana oocyte ribonuclease; RaCOR1; CD22; covalently bound; LL2 antibody; ligand binding molety; cancerous B cell; Kaposi's sarcoma; human chorionic gonadotrophin; hCG; signal peptide; recombinant ribonuclease; cytotoxic fusion protein; cancer; bullfrog;
cytotoxic fusion proteins. They can be used for treatment of cancer and
                                                                                                                                                                         QNWATFQQKHIINTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNVL
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                                                                                                                       Gaps
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                                                                                                                                                                                                                       STTRFQLNTCTRISITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
                                                                                                                     ;0
                                                                                 Length 110;
                                                                                                                                                                                                                                           STTRFQLNTCTRTSITPRPCPXSSRTETNYICVKCENOYPVHFAGIGRCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note= "Met not found in wild type RaCOR1"
                                                                                                                   0; Indels
                                                                                 100.0%; Score 602; DB 2; 100.0%; Pred. No. 6.1e-61;
                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (USSH ) US DEPT HEALTH & HUMAN SERVICES.
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                                                                                                                                                                                                                                                                                                                                         AAY28873 standard; protein; 111 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 22; Page 63; 71pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99WO-US006641
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Recombinant Met(-1) RaCOR1
                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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                                                                                                                   Matches 110; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1999-610847/52.
N-PSDB; AAZ08131.
                   autoimmune diseases
                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rana catesbeiana.
                                                   Sequence 110 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9950398-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                           25-JAN-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic
                                                                                                                                                                                                                       61
                                                                                                                                                                                                                                                                                                                                                                         AAY28873;
                                                                                 Query Match
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human
                                                                                                                                                                                                                                                         Recombinant Rana catesbeiana oocyte ribonuclease; RacOR1 Gln1Ser; CD22; covalently bound; LL2 antibody; ligand binding moiety. cancerous B cell; bullfrog; Kaposi's sarcoma; human chorionic gonadotrophin; hCG; RNase; signal peptide; recombinant ribonuclease; cytotoxic fusion protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is a recombinant Rana catesbelana oocyte ribonuclease (RaCOR1) protein with Gln1Ser. Carboxy terminal end of recombinant RaCOR1 has a covalently bound ligand binding moiety, which can be a Li2 antibody directed against CD22 on cancerous B cells or huma chorionic gonadotrophin (hCG) effective against Kaposi's sarcoma cells. Recombinant ribonucleases can be expressed in bacteria without an Neterminal methionine due to the presence of a signal peptide that is cleaved by bacteria. The soluble expression of ribonuclease allows the proteins to be fused in-frame with ligand binding moieties to form cytotoxic fusion proteins. They can be used for treatment of cancer and autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New recombinant ribonucleases, used for killing target cells, e.g. for treating cancers, viral infections or autoimmune diseases.
61 STTRFQLNTCTRISITPRPCPYSSRTEINYICVKCENQYPVHFAGIGRCP 110
                  STTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "Wild type Gln replaced with Ser"
                                                                                                                                                                                                                        Recombinant RaCOR1 Gln1Ser amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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                                                                                                                    AAY28877 standard; protein; 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98US-0079751P.
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                                                                                                                                                                                                                                                                                                                                  cancer; autoimmune disease
                                                                                                                                                                                         entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (USSH ) US DEPT HEALTH
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Misc-difference
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Length 110;

2;

DB

Score 597;

99.2%;

Query Match

autoimmune diseases

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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
                     Copyright
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- protein search, using sw model OM protein

7, 2004, 21:25:55 ; Search time 46.9224 Seconds (without alignments) 662.376 Million cell updates/sec May о :: Run

602 1 ONWAIFQOKHIINTPIICNT.....ICVKCENQYPVHFAGIGRCP 110 Perfect score: Sequence:

US-09-961-400-15

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1586107 Total number of hits satisfying chosen parameters:

1586107 seqs, 282547505 residues

Searched:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Maximum Match 100% Listing first 45 summaries Post-processing: Minimum Match 0%

geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* geneseqp2004s:* A_Geneseq_29Jan04:* geneseqp1980s:* geneseqp1990s:* geneseqp2000s:* geneseqp2001s:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Aay28872 Rana cate	Recom					Aay33321 Frog lect		Aay28865 Rana pipi	Recon			Aay28869 Recombina			Abg32650 Northern	Rec		Aay28870 Recombina		Aar12344 Protein w	Aar47303 ONCONASE	Aaw00736 Protein d	Aaw14065 Onconase	Aaw06543 Antitumou
DI	AAY28872	AAY28873	AAY28877	AAY28878	AAY28874	AAY28876	AAY33321	AAW06544	AAY28865	AAY28867	AAY28879	AAY28866	AAY28869	AAW30301	AAB31666	ABG32650	AAY39400	AAW35126	AAY28870	AAY28871	AAR12344	AAR47303	AAW00736	AAW14065	AAW06543
D.B	2	N	C)	C)	C)	C)	N	N	7	7	0	7	7	N	4	Ŋ	N	N	~≀	0	7	7	N	7	7
% Query Match Length	110	111	110	111	110	111	111	104	104	105	127	104	105	104	104	104	105	379	104	105	104	104	104	104	104
% Query Match	100.0	100.0	99.2	99.5	0.66	0.66	97.8	47.3	46.8	46.8	46.8	46.3	46.3	46.1	46.1	46.1	46.1	46.1	45.9	•	45.6	45.6	45.6	45.6	45.6
Score	602	602	597	597	296	9	•	284.5	281.5	281.5	281.5	278.5	278.5	277.5	277.5	277.5	277.5	277.5	276.5	76.	274.5	74.	274.5	274.5	274.5
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AAW88233 AAY33322 AAW35123	AAW35125 AAW35130 AAB31667	ABG31617 AAW35122 AAW35117	AAW35118 AAW35134 AAW35135	AAW35133 AAW35129 AAW35132	AAW30302 AAW18224 AAW35115	AAW35116 AAW35127
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104 104	355 358 104	104	112 251	322 325 366	104	105 358
4.45.6 6.5.6 6.5.6	45.6 45.6 3.3	4 4 4 7 7 4 8	44 44 6 7 6 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	4.4.4.4.4.4.4.4.4.4.4.4.4.4.4.4.4.4.4.	44.4
274.5	274.5 274.5 272.5	272.5	272.5 272.5	272.5 272.5 272.5 272.5	271.5 267.5 267.5	267.5 263.5
55 52 53 53 54		0 0 0 0 0 4 0 0 4	35 36 37	2 6 6 4 8 6 0	4 4 4 1 2 8	4.4 5.5

ALIGNMENTS

Rana catesbeiana oocyte ribonuclease, RaCOR1; covalently bound; CD22; L2 antibody, Higand binding moiety, cancerous B cell; Raposi's Sarcoma; human chorionic gonadotrophin; hG3; recombinant ribonuclease; bullfrog; signal peptide; cytotoxic fusion protein; cancer; autoimmuse disease; Rana catesbeiana oocyte ribonuclease (RaCOR1) amino acid sequence. AAY29872 standard; protein; 110 AA (first entry) 25-JAN-2000 AAY29872; RESULT 1 AAY28872 HANDER STANDER
Rana catesbeiana. Synthetic.

WO9950398-A2

07-OCT-1999.

99WO-US006641. 26-MAR-1999; (USSH) US DEPT HEALTH & HUMAN SERVICES.

98US-0079751P

27-MAR-1998;

Newton DL; Rybak SM,

WPI; 1999-610847/52. N-PSDB; AAZ08130.

New recombinant ribonucleases, used for killing target cells, e.g. for treating cancers, viral infections or autoimmune diseases.

Claim 22; Page 62; 71pp; English.

The present sequence is a Rana catesbeiana oocyte ribonuclease (RacOR1) protein encoded by a cDNA modified for expression in E. coli. Carboxy terminal end of RacOR1 has a covalently bound ligand binding moiety, which can be a LL2 antibody directed against CD22 on cancerous B cells or human chorionic gonadotrophin (hCG) effective against Kaposi's Sarcoma cells. Recombinant ribonucleases can be expressed in bacteria without an N-terminal methionine due to the presence of a signal peptide that is cleaved by bacteria. The soluble expression of ribonuclease allows the proteins to be fused in-frame with ligand binding moieties to form

Search completed: May 7, 2004, 21:53:05 Job time : 5.30402 secs

8 P P

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                                                                                                                                                                                      IASKNVL------TISEFYLSDCNVTSRP----CKYKLKKSTNTFCVTCENQ--AP 96
                                                                                                                            SDWLTFQKKHL-----INTRDVDCNNIM---SINLFHCKDKNTFIYSRPEPVKAICKGI
                                                                                                                                                3 SSAMKFQRQHMDPEGSPSNSSNY-CNVMMIRRNWTQGRCKPVNTFVHESLADVQAVC---
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Hystricognathi; Echimyidae; Proechimys.
NCBI_TaxID=10163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Meditems 3.7., Knol G., Antens B.,

Beithems J.J., Knol G., Antens B.,

The primary structures of pancreatic ribonucleases from African

T porcupine and casiragua, two hystricomorph rodent species.";

Biochim. Biophys. Acta 705:102-110(1982).

C -!- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-

phosphates and 3'-phosphate intermediates.

C --- SUBCELMULAR LOCATION: Secreted.

C --- SUBCELMULAR LOCATION: Secreted.

C --- SUBLINIAR LOCATION: Pancreas.

C --- SUBLIAR LOCATION: Recreted.

R RSP; PO0656; ISRN.

R INTERPROJECT: RASEA.

R PFRO074; rnaseA; I.

R PRINTS; RR0074; RIBONUCLEASE.

R PLODEN: PROOFS; RNASEA; I.

R PLODEN: PROOFS; RNASEA; I.

R PLODEN: PROOFS; RNASEA; I.
                                                                                                  30; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20.6%; Score 120; DB 1; Length 128; 29.9%; Pred. No. 5e-06;
                                                                    20.6%; Score 120; DB 1; Length 128; 28.5%; Pred. No. 5e-06; tive 21; Mismatches 37; Indels
                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1986 (Rel. 03, Created)
01-NOV-1986 (Rel. 03, Last sequence update)
01-Roy (Rel. 41, Last annotation update)
Ribonuclease pancreatic (EC 3.1.27.5) (RNase 1) (RNase A).
RNASE1 OR RNS1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36; Indels
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2DB58093A9D3C936 CRC64;
                                         A2F4101A1A33E93B CRC64;
N-LINKED (GLCNAC. . .).
N-LINKED (GLCNAC. . .).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hydrolase; Nuclease; Endonuclease; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-LINKED (GLCNAC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SM00092; RNASe_PC; 1.
PROSITE; PS00127; RNASE_PANCREATIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=83000399; PubMed=7115727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94 B1 B1 12 B1 12 B1 12 B1 12 B1 14 B1 B1 14 B1 B1 14 B1 B1 14 B1 14 A1 B1 14 AW
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21 N-
34 N-
64 L
14406 MW;
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                                                                                                  35; Conservative
                                                                                                                                                                                                                                                                                                                                                  STANDARD;
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128 AA;
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                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rissue=Pancreas;
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                                            SEQUENCE
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 CARBOHYD
                              VARIANT
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RNP PROGU
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7 FOKKHL-----TUTRDVDCNNIM-STNLF--HCKDKNTFIYSRPEPVKAICKGIIASKNV 58

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

STATIS-FUBLNIA INSECUE.

STATIS-FUBLNIA INSECUE.

STATIS-FUBLNIA INSECUE.

MEDLINE=22388257; PubMed=1247,932;

Altschul S.F., Zeeberg B. T., Grouse L.H., Derge J.G.,

Rlausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Hand D., Haibe F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Toshiyuki S., Carninci P., Prange C.,

Brownstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Willialon D.K., Muray D.W., Schergren B.J., Lu X., Gibbs R.A.,

Willian A., Touchman J.W., Shevchenko Y., Bouffard G.G.,

Rab Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rab Blakesley R.W., Krzywinski M.I., Skalska U., Smailus D.E.,

Rab Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,

Rab and dinitial analysis of more than 15,000 full-length

Rab Human and mouse colly sequences.",
Biochim. Biophys. Acta 1162:177-186(1993).

-!- FUNCTION: May function as a tRNA-specific ribonuclease that binds to actin on the surface of endothelial cells; once bound, angiogenin is endocytosed and translocated to the nucleus, thereby promoting the endothelial invasiveness necessary for blood vessel formation. Angiogenin induces vascularization of normal and malignant tissues. Abolishes protein synthesis by specifically hydrolyzing cellular tENAs.
-!- SUBCELPULAR LOCATION: Secreted.
                                                                                                     64 PCKNGQSNCYESTSNWHITDCRLTSNSKFPDCLYRTSQEEKSIIVACEGNPYVPUHF 120
                                                                        59 -----LITSEFYLSDCNVTSR----PCKYKLKKSINTFCVTCENQ--APVHF 99
                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=93192291; PubMed=8448182;
Bond M.D., Strydom D.J., Vallee B.L.;
"Characterization and sequencing of rabbit, pig and mouse
angiogenins: discernment of functionally important residues and
                                                                                                                                                                                                                                                                                     01-MAY-1991 (Rel. 18, Created)
01-MAY-1991 (Rel. 18, Last sequence update)
15-MAY-2004 (Rel. 43, Last annotation update)
Angiogenin precursor (EC 3.1.27.-) (Ribonuclease 5) (RNase 5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: Belongs to the pancreatic ribonuclease family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIJNE=91025023; PubMed=2222458;
Bond M.D., Vallee B.L.;
"Isolation and sequencing of mouse angiogenin DNA.";
Biochem. Biophys. Res. Commun. 171:988-995(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     roc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                            145
                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                 5 LIFOKKHLINIRDVD-----CHNIMSTNLF---HCKDKNTFIYSRPEPVKAICKGIIASK 56
                                                                                                                                                                                                                                                                                                                   62 NVLCKNGRINCYESNSIMHIIDCRQIGSSKYPNCAVKISQKEKHIIVACEGNPYVPVHF 120
                                                                                                                                                                                                                                                                                                                                                        NVL------TISEFYLSDCNVTSRP----CKYKLKKSINTFCVTCENQ--APVHF 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mol. Biol. Evol. 19:438-445(2002).

-!- FUNCTION: May function as a tRNA-specific ribonuclease that binds to actin on the surface of endothelial cells; once bound, angiogenin is endocytosed and translocated to the nucleus, thereby promoting the endothelial invasiveness necessary for blood vessel formation. Angiogenin induces vascularization of normal and malignant tissues. Abolishes protein synthesis by specifically hydrolyzing cellular ENRAs (By similarity).
                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zhang J., Rosenberg H.F.; "Diversifying selection of the tumor-growth promoter angiogenin in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Macaca mulatta (Rhesus macaque).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Cercopithecidae,
                                                                                                                                                                                                                                                                            28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Anglogenin precursor (EC 3.1.27.-) (Ribonuclease 5) (RNase 5)
                                                                                                                                                                                                                                                  Length 124;
                                                                                                                                                                                                      76 N-LINKED (GLCNAC. .) (30%).
14125 MW; F57475459F697B20 CRC64;
                                                                                                                                                                                                                                                                           42; Indels
InterPro; IPkuul,

Pfam; PF00074; rnaseA; 1.

R PRINTS; PR00794; RIBONUCLEASE.

R PROMO92; RNASe Pc; 1.

R PROSITE; PS00127; RNASE PANCREATIC; 1.

R Hydrolase; Nuclease; Endonuclease; Glycoprotein.

R PATTOLASE; PS00127; RNASE PANCREATIC; 1.

R PROSITE; PS00127; RNASE PANCREATIC; 1.

R PROSITE; PS00127; RNASE PANCREATIC; 1.

R PRINILARITY.

BY SIMILARITY.

BY SIMILARITY.
                                                                                                                                                                                                                                                           Pred. No. 1.4e-06;
                                                                                                                                                                                                                                               Score 125; DB 1;
                                                                                                                                  SIMILARITY.
SIMILARITY.
SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          146 AA
                                                                                                                                                                                                                                                                         15; Mismatches
                                                                                                                                                                          SIMILARITY
SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=21918422; PubMed=11919285;
                                                                                                        BY
BY
BY
BY
BY
BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-FEB-2003 (Rel. 41, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF441667; AAL61649.1; -
                                                                                                                                                                                                                                               21.5%;
                                                                                                                                                                                                                                                           28.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001427; RNaseA.
Pfam; PF00074; rnaseA; 1.
                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cercopithecinae; Macaca.
                                                                                                                   95
110
72
12
41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           primate evolution.";
                                                                                                                                                                                                                    124 AA;
                                                                                                                                                                                                                                                           Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9544;
                                                                                                                                  58
65
12
41
119
76
                                                                                                                                                                                                                                                                       34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ANGI MACMU
Q8WN63;
                                                                                                                                                         ACT SITE
ACT SITE
ACT SITE
                                                                                                                                                                                                                                                                                                                              ø
                                                                                                                                                                                                                                                                                                                                                        57
                                                                                                                                               DISULFID
                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                   CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                        ANGI MACMU
                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 12
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PRINTS; PR00794; RIBONUCLEASE.

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                                                                                                                                                                                                                                                                                                    6 TFQKKHLINIRDVDCNNIMSTNLFHCKDKNTFIYSRPBPVKAIC---KGIIASKNV-LIT
                                                                                                                                                                                                                                                           23; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Pancreas;
MEDLINE=77185022; PubMed=862624;
Wan den Berg A., van den Hende-Timmer L., Hofsteenge J., Gaastra W.,
Van den Besintema J.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Guinea-pig pancreatic ribonucleases. Isolation, properties, primary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             structure and glycosidation.";
Eur. J. Blochem. 75:91-100(1977).
-!- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
phosphates and 3'-phosphooligonucleotides ending in C-P or U-P
with 2',3'-cyclic phosphate intermediates.
-!- SUBCELLULAR LOCATION: Secreted.
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
28-FIBS-2003 (Rel. 41, Last annotation update)
Ribonuclease pancreatic B (EC 3.1.27.5) (RNase IB).
Cavia porcellus (Guinae pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                               Length 146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -i- SIMILARITY: Belongs to the pancreatic ribonuclease family. PIR; A00826; NRGPB.
                                                                                         PYRROLIDONE CARBOXYLIC ACID (B SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                      E39A89215DB2A2A4 CRC64;
                                                                                                                                                                                                                                                                                                                                                      98
                                                                                                                                                                                                                                  .5;
.4e-06;
.32;
                                                                                                                                                                                                                                                                                                                                    62 SEFYLSDCNVTS----RPCKYKLKKSTNTFCVTCENQAPVH
                                                                                                                                                                                                                                DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hydrolase; Muclease; Endomolease; Glycoprotein.

DISULFID 40 95 BY SIMILARITY.

DISULFID 58 110 BY SIMILARITY.

DISULFID 65 72 BY SIMILARITY.

ACT_SITE 12 BY SIMILARITY.

ACT_SITE 11 BY SIMILARITY.

ACT_SITE 11 BY SIMILARITY.

ACT_SITE 11 BY SIMILARITY.
                                                                                                                                                                                                                                                        17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                    128 AA
                                                                                                                                                                                                                               20.9%; Score 121.5;
                                                                                                                                                                                                                                             No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSSP; P00656; ISRN.
InterPro; IPR001427; RNaseA.
Pfam; PF00074; rnaseA; 1.
PRINTS; PR00794; RIBONUCLEASE.
ProDom; P0000535; RNaseA; 1.
SWART; SM00092; RNASe_PC; 1.
PROSITE; PS00127; RNASE_PANNEATIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                              Pred
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -! - TISSUE SPECIFICITY: Pancreas
                                                                                                                                                                                                   16301 MW;
                                                                                                                                                                                                                                             28.78;
                                                                                                                                                                                                                                          Local Similarity 28.7%
les 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                   37
64
138
105
116
131
                                                                                                                                                                                                   146 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10141;
                                                                                                                                                                                                                                                                                                                                                                                                                                RNPB CAVPO
                                                                                                                   ACT_SITE
ACT_SITE
ACT_SITE
DISULFID
                                                                                                                                                                       DISULFID
DISULFID
SEQUENCE
                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 13
RNPB_CAVPO
                                                                                                                                                                                                                                                    Matches
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Ξ

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7 FOKKHL-----TNTRDVDCNNIM-STNLF--HCKDKNTFIYSRPEPVKAICKGIIASKNV 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8 FERQHMDSRGSPSTNPNYCNEMMKSRNMTQGRCKPVNTFVHEPLADVQAVC----FQKNV 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64 LCKNGQTNCYQSNSNMHITDCRVTSNSDYPNCSYRTSQEEKSIVVACEGNPYVPVHF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59 L-----TISEFYLSDCNVTSRP----CKYKLKKSTNTFCVTCENO--APVHF 99
TISSUE=Pancreas;
MEDIATR=7705676, PubMed=999896,
MEDIATR=7705676, van den Hende-Timmer L., Beintema J.J.;
"Isolation, properties and primary structure of coypu and chinchilla pancreatic ribonuclease.";
Biochim. Biophys. Acta 453:400-409(1976).
-!- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-phosphotaes and 3'-phosphotoligonucleotides ending in C-P or U-P with 2',3'-cyclic phosphate intermediates.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Emmens M., Welling G.W., Beintema J.J., "The amino acid sequence of pike-whale (lesser-rorqual) pancreatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Balaenoptera acutorostrata (Minke whale) (Lesser rorqual).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Cetacea; Mysticeti;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Blochem. J. 157:317-323 (1976).
-!- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside phosphates and 3'-phosphooligonucleotides ending in C-P or with 2',3'-cyclic phosphate intermediates.
-!- SUBCELULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Pancreas.
-!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
                                                                                                                                                                                                                          -i- TISSUE SPECIFICITY: Pancreas.
-i- SIMILARITY: Belongs to the pancreatic ribonuclease family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P00673;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Ribonuclease pancreatic (EC 3.1.27.5) (RNase 1) (RNase A)
RNASE1 OR RNS1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-LINKED (GLCNAC. . ).
4EB924E52B445832 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS0012/; KNASE FANCAGES.

Hydrolase; Nuclease; Endonuclease; Glycoprotein.

DISULFID 26 84 BY SIMILARITY.

DISULFID 40 95 BY SIMILARITY.

DISULFID 65 72 BY SIMILARITY.

ACT SITE 41 41 BY SIMILARITY.

ACT SITE 119 119 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; DB 1;
1.1e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               124 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21.6%; Score 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                  PANCREATIC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=76277855; PubMed=962870;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84 BY
195 BY
110 BY
72 BY
12 BY
41 BY
34 NV
14267 MW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Balaenopteridae; Balaenoptera.
                                                                                                                                                                                                                                                                                                                                    Pfam; PF00074; rnaseA; 1.
PRINTS; PR00794; RIBONUCLEASE.
ProDom; PD000535; RNaseA; 1.
                                                                                                                                                                                                                                                                                              HSSP; P00656; 1SRN.
InterPro; IPR001427; RNaseA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29.9%;
                                                                                                                                                                                                                                                                                                                                                                                                          SMART; SM00092; RNASe PC; 1
PROSITE; PS00127; RNASE_PAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           l Similarity 29.9
35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                         PIR; A00822; NRCU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9767;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ribonuclease.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RNP BALAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 q
       δ
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                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5
                                                                                                                                                                                                                                                                                                                                                                                                                                  noved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99
                            resonance spectroscopy.";
Biochemistry 35:8870-8880(1996).
Biochemistry 35:8870-8880(1996).
Lo actin on the surface of endothelial cells; once bound, angiogenin is endocytosed and translocated to the nucleus, thereby angiogenin is endocytosed and translocated to the nucleus, thereby promoting the endocytosed and translocated to the nucleus, thereby promoting the endochelial invasiveness necessary for blood vessel formation. Angiogenin induces vascularization of normal and mailgnant tissues. Abolishes protein synthesis by specifically hydrolyzing cellular triNAs. Binds tightly to placental ribonuclease inhibitor and has very low ribonuclease activity.
-: SINGELEGITY: Secreted.
-: SINIARITY: Belongs to the pancreatic ribonuclease family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DVDCNNIMSTNLF--HCKDKNTFIYSRPEPVKAICKGIIASKN------VLTTSEFYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Būkaryota; Metazoa; Čhordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Hystricognathi; Myocastoridae;
       "Solution structure of bovine angiogenin by 1H nuclear magnetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22.0%; Score 128; DB 1; Length 148; 34.0%; Pred. No. 8.3e-07; ive 14; Mismatches 32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-JUL-1986 (Rel. 01, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Ribonuclease pancreatic (EC 3.1.27.5) (RNase 1) (RNase A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16969 MW; B7999124CBB523DD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 103 TICKHKGGSSRPPCRYGATEDSRVIVVGCENGLPVHF 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SWART; SM00092; RNAse_Pc; 1.
PSOSITE; PSO0127; RNASE_PANCREATIC; 1.
Hydrolase; Nuclease; Endonuclease; Angiogenesis;
Protein synthesis inhibitor; Signal; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67 SDC---NVTSR-PCKYKLKKSTNTFCVTCENQAPVHF 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ANGIOGENIN-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (S. or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Myocastor coypus (Coypu) (Nutria).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001427; RNaseA.
PEfan; PF00074; TRBGAS, 1.
PRINTS; PR00794; RIBONUCLEASE.
ProDom; PD000535; RNaseA. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-JUL-1986 (Rel. 01, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF135124; AAG47631.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PDB; 1AGI; 03-APR-96.
PDB; 1GIO; 07-DEC-96.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             148 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RNASE1 OR RNS1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RNP_MYOCO
P00676;
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ACT_SITE ACT_SITE

SIGNAL CHAIN

DISULFID

DISULFID SEQUENCE Query Match

Best Local

17

à a à d PIR; A00818; NRWHK HSSP; P00656; 1SRN

NCBI_TaxID=10157;

Myocastor [1] SEQUENCE.

RNP_MYOCO

1D RNP M

AC 21-JU

DT 21-JU

DT 21-JU

DT 21-JU

DT 21-JU

DT 21-JU

DT 21-JU

DT 21-JU

DT 21-JU

DT 21-JU

DT 21-JU

DT 21-JU

DT 21-JU

DT 21-JU

DT 21-JU

DT 21-JU

DT 21-JU

DT 21-JU

RNASE

OC MAMMA

RESULT 10

Gaps

28;

36; Indels

Length 128;

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ACT_SITE
ACT_SITE
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DISULFID
                                                              DISULFID
                                                                                                                                                                                                                                                                       86
                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                         BOVIN
       SHIFFF
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                                                                                                                                                                                            63 CKDVNTFIHDTKNNIKAICGKKGSPYGRNLRISKSRFQVTTCTHKGRSPRPPCRYRASKG 122
                                                                                                                                                                              83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zhang J., Rosenberg H.P.;

"Diversifying selection of the tumor-growth promoter angiogenin in primate evolution.";

Mol. Biol. Evol. 19:438-445(2002).

-!- FUNCTION: May function as a tRNA-specific ribonuclease that binds to actin on the surface of endothelial cells; once bound, angiogenin is endocytosed and translocated to the nucleus, thereby promoting the endothelial invasiveness necessary for blood vessel formation. Angiogenin induces vascularization of normal and malignant tissues. Abolishes protein synthesis by specifically hydrolyzing cellular tRNAs (By similarity).

-!- SUBCELIULAR LOCATION: Secreted.

-!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
                                                                                                                                                                              --- PCKYKLKKS
                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Verrebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
Cercopithecinae, Cercopithecus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; Lruv....,
Pfam; PF00074; maseA; 1.
PRINTS, PR00794; RIBONULEASE.
PRODOM; PD000535; RNaseA; 1.
SMART; SM0092; RNASe Pc; 1.
PROSITE; PS00127; RNASE Pc; 1.
Hydrolase; Nuclease; Endonuclease; Anglogenesis;
Protein synthesis inhibitor; Signal; Pyrrolidone carboxylic acid.
Protein synthesis inhibitor; Signal; Pyrrolidone carboxylic acid.
Broteen
                                                                                                                                                7;
                                                                                                                  22.4%; Score 130.5; DB 1; Length 145; 38.2%; Pred. No. 4.4e-07; live 11; Mismatches 29; Indels 7
                                                                                                                                                                                                                                                                                                                                                               28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last amnotation update)
Anglogenin precursor (EC 3.1.27.-) (Ribonuclease 5) (RNase 5)
ANG OR RNASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ANGIOGENIN.
PYRROLIDONE CARBOXYLIC ACID (BY
                                                                                                                                                                        31 CKDKNTFIYSRPEPVKAIC--KGIIASKNV-LTTSEFYLSDCNVTSR
                                                                       Y SIMILARITY.
29A6EB814429C4AD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Cercopithecus aethiops (Green monkey) (Grivet)
                SIMILARITY.
SIMILARITY.
SIMILARITY.
                                                                                                                                                                                                                                                                                                                                      146 AA.
   SIMILARITY
                                                           SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY)
                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=21918422; PubMed=11919285;
   BY
BY
BY
BY
BY
                                                                                     16612 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF441664; AAL61646.1; -.
InterPro; IPR001427; RNaseA.
                                                                                                                                                                                                                                                             123 FRYIIIGČENGWPVHF 138
                                                                                                                                                                                                                                  84 INTECVICENQAPVHF 99
                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                     STANDARD;
 37
64
137
104
115
                                                                                        A.
                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
37
64
137
50
63
81
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                                                                                                                                             29;
                                                                                                                                                                                                                                                                                                                                     ANGI CERAE
            ACT_SITE
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                                                                                                                                  Local
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MOD RES
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61
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53 TMRRRHLTSP------CKDINTFIHGNRHHIKALCGDENGNPYGENLRISK 97
                                                                                                                                             6 TFQKKHLINTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAIC---KGIIASKNV-LTT
                                                                                                                        23; Gaps
                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Maes P., Damart D., Rommens C., Montreuil J., Spik G., Tartar A.; "The complete amino acid sequence of bovine milk angiogenin."; FEBS Lett. 241:41-45(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bond M.D., Vallee B.L., "Isolation of bovine angiogenin using a placental ribonuclease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=95224057; PubMed=7708754;
Acharya K.R., Shapiro R., Riordan J.F., Vallee B.L.;
"Crystal structure of bovine angiogenin at 1.5-A resolution.";
Proc. Natl. Acad. Sci. U.S.A. 92:2949-2953 (1995).
                                                                                                  Length 146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and expression of bovine angiogenin."; to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRUCTURE BY NMR.
MEDLINE=96280645; PubMed=8688423;
Lequin O., Albaret C., Bontems F., Spik G., Lallemand J.-Y.;
                                                                                                                          Indels
                                                                       27860112E85B8DF9 CRC64;
                                                                                                                                                                                                              98
                                                                                                                                                                                              62 SEFYLSDCNVTS----RPCKYKLKKSTNTFCVTCENQAPVH
                                                                                                 DB 1;
                                                                                                                        17; Mismatches 30;
                                                                                                             4.4e-07;
                                                                                                                                                                                                                                                                           Bond M.D., Strydom D.J.;
"Amino acid sequence of bovine angiogenin.";
Biochemistry 28:6110-6113(1989)
                                  SIMILARITY.
SIMILARITY.
SIMILARITY.
  SIMILARITY
            SIMILARITY
                                                                                                Score 130.5;
Pred. No. 4.4
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 BY
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BY
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                                                                         16444 MW;
                                                                                               22.4%;
                                                                                           Query Match 22.4%
Best Local Similarity 30.7%
Matches 31; Conservative
37
64
138
105
116
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Submitted (MAR-1999) t
                                                                                                                                                                                                                                                                                                                                                                     Bos taurus (Bovine).
37
64
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146 AA;
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84
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110
72
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MOD_RES
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    SPETEFF
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"Origin of the duplicated ribonuclease gene in guinea-pig: comparison of the amino acid sequences with those of two close relatives:

"Origin of the amino acid sequences with those of two close relatives:

"I of the amino acid sequences with those of two close relatives:

"I wol. Evol. 19:145-122 (1983).

"I MOI. Evol. 19:145-122 (1983).

"I MOSSPARCE ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-phosphates and 3'-phosphoulgonucleotides ending in C-P or U-P with 2' 3'-cyclic phosphate intermediates.

"I SUBCLEGILLAR LOCATION: Secreted.

"I TISSUE SPECIFICITY: Pancreas.

"I SIMILARITY: Belongs to the pancreatic ribonuclease family.

R PIRF, AO0857; NRU.

R HSSP: PO0656; 1SRN.

InterPro; IPR001427; RNASEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 DWSSFQNKHIDYPETSASNPNAYCDLAMQRRNINPTKCKTRNTFVHASPSEIQQVCGSGG 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 DWLTFQKKHL-----TNTRDVDCNNIM---STNLFHCKDKNTFIYSRPEPVKAIC--KG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                 HSSP, PO0655,
A InterPro; IPR001427; ...
B Fina, PR00074; rnaesA; 1.
DR PRINTS; PR00794; RIBONUCLEASE.
DR PRINTS; PR00052; RNaesA; 1.
DR PROSITE; PS00127; RNASE PC; 1.
DR Hydrolase; Dadounclease; Pyrrolidone carboxylic acid.
FT MOD RES 1 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT DISULPID 25 80 BY SIMILARITY.
FT DISULPID 39 91 BY SIMILARITY.
FT DISULPID 57 106 BY SIMILARITY.
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FT TOTAL STATEMENTY.
FT TOTAL STATEM
-!- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
phosphates and 3'-phosphooligonucleotides ending in C-P or U-P
with 2',3'-oyclic phosphate intermediates.
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Pancreas.
-!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
PIR; 941111; 941111.
HSSP; P00656; 1LSQ.
InterPro; IRR01427; RNaseA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62 THYEDNLYDSNESFDLTDCKNVGGTAPSSCKYNGTPGTKRIRIACENNQPVHF 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52 IIASKNVLTTSE-FYLSDC----NVTSRPCKYKLKKSTNTFCVTCENQAPVHF 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Galea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24.7%; Score 144; DB 1; Length 119; 30.1%; Pred. No. 1.3e-08; ive 19; Mismatches 44; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-JUL-1986 (Rel. 01, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Ribonuclease pancreatic (EC 3.1.27.5) (RNase A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            124 AA
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PROSITE; PS00127; RNASE PANCREATIC; 1.
Hydrolase; Nuclease; Endonuclease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=87036770; PubMed=6571219;
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PRINTS; PR00794; RIBONUCLEASE.
ProDom; PD000535; RNaseA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last seq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
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P00680;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                  SDWLTFQKKGHL-----TNTRDVDCNNIM---STNLFHCKDKNTFIYSRPEPVKAICKG 51
                                                                                                                                                                                                                                                                        3 SSAMKFÖRQHMDSDGHPDTNTN--YCNEMMVRRSMTOGRCKPVNTFVHEPLEAVQAVC-- 58
                                                                                                                                                                                                                                                                                                              52 IIASKNV-----LITISEFYLSDCNVTSRP----CKYKLKKSTNTFCVTCEN--QA 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRALM-129, TISSUE-Liver;
STRALM-129, TISSUE-Liver;
MEDLINE-56079109; PubMed-8530072;
Brown W.E., Nobile V., Subramanian V., Shapiro R.;
Brown W.E., Nobile V., Subramanian V., Shapiro R.;
"The mouse angiogenin gene family: structures of an angiogenin-related genomics 29:200-206(1995).
                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                          32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
                                                                                                                  MISSING (IN 1/3 OF THE MOLECULES) 609C7E251A7BBA25 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANGIOGENIN-RELATED PROTEIN.
PYRROLIDONE CARBOXYLIC ACID (BY
                                                                                                                                                                    ; Score 132; DB 1; Length 124;
; Pred. No. 2.5e-07;
18; Mismatches 36; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
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SIMILARITY.
SIMILARITY.
SIMILARITY.
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PRINTS; PR00794; RIBONUCLEASE.
PPCDOM; PD000535; RNaseA; 1.
SMART; SM00092; RNASE PC; 1.
PR0SITE; PS00127; RNASE PANCREATIC; 1.
Signal; Hydrolase; Nuclease; Pyrrolidone carboxylic acid.
                                                                                   SIMILARITY.
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 BY
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                                                                                                                                      13870 MW;
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InterPro; IPR001427; RNaseA.
                                                                                                                                                                         22.7%;
30.6%;
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                                                                                                                                                                                                            38; Conservative
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RNP_IGUIG
P80287;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
DWLTFQKKHLTNTRDVDCNNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKNV
                                      J. Biochem. 108:139-143(1990).
-!- FWOVTION: The S-lectins in frog eggs may be involved in the fertilization and development of the frog embryo. This lectin preferentially agglutinate a large variety of tumor cells, but it does not agglutinate non-transformed cells and erythrocytes.
-!- SUBGELIULAR LOCATION: Secreted.
-!- SUBCILIULAR LOCATION: Secreted.
-!- STATIARRIY: Belongs to the pancreatic ribonuclease family.
PIR: JX0120: JX0120.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kamiya Y., Oyama F., Oyama R., Sakakibara F., Nitta K., Kawauchi H.,
Takayanagi Y., Titani K.;
"Amino acid sequence of a lectin from Japanese frog (Rana japonica)
                                                                                                                                                                                                                                                                                                                                                                01-NOV-1990 (Rel. 16, Created)
01-FBB-1994 (Rel. 28, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Sialic acid-binding lectin (EC 3.1.27.-).
Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Rana: Annura; Rebatrachia; Ranidae; Rana: Manghata; Anura; Rebatrachia; Ranidae; Rana: Mangalana; Rana: Mangalana; Rana: Mangalana; Rana: Mangalana; Mangalana; Rana: Mangalana; Mangalana; Rana: Mangalana; Mangalana; Rana: Mangalana; Mangalana; Mangalana; Mangalana; Mangalana; Mangalana; Mangalana; Mangalana; Mangalana; Mangalana; Mangalana; Mangalana; Mangalana; Mangalana; Mangalana; Mangalana; Mangalana; Mangalana; Mangalana; Mangalana; Mangalana; Mangalana; Mangalana; Mangalana; Mangalana; Mangalana; Mangalana; Mangalana; Mangalana; Mangalana; Mangalana; Mangalana; Mangalana; Mangalana; Mangalana; Mangalana; Mangalana; Mangalana; Mangalana; Mangalana; Mangalana; Mangalana; Mangalana; Mangalana; Mangalana; Mangalana; Mangalana; Mangalana; Mangalana; Mangalana; Mangalana; Mangalana; Mangalana; Mangalana; Mangalana; Mangalana; Mangalana; Mangalana; Mangalana; Mangalana; Mangalana; Mangalana; Mangalana; Mangalana; Mangalana; Mangalana; Mangalana; Mangalana; Mangalana; Mangalana; Mangalana; Mangalana; Mangalana; Mangalana; Mangalana; Mangalana; Mangalana; Mangalana; Mangalana; Mangalana; Mangalana; Mangalana; Mangalana; Mangalana; Mangalana; Mangalana; Mangalana; Mangalana; Mangalana; Mangalana; Mangalana; Mangalana; Mangalana; Mangalana; Mangalana; Mangalana; Mangalana; Mangalana; Mangalana; Mangalana; Mangalana; Mangalana; Mangalana; Mangalana; Mangalana; Mangalana; Mangalana; Mangalana; Mangalana; Mangalana; Mangalana; Mangalana; Mangalana; Mangalana; Mangalana; Mangalana; Mangalana; Mangalana; Mangalana; Mangalana; Mangalana; Mangalana; Mangalana; Mangalana; Mangalana; Mangalana; Mangalana; Mangalana; Mangalana; Mang
                                                                                                               59 LITSEFYLSDC---NVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
                                                                                                                                                  7;
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PROSITE; PS00127; RNAŠE PANCREATIC; 1.
Hydrolase; Nuclease; Endomuclease; Sialic acid; Lectin;
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                                                                                                                                                                                                                                                                                                                       PRT;
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Pfam; PF00074; rnaseA; 1.
ProDom; PD000535; RNaseA; 1.
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52
94
111 AA;
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Best Local Similarity
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ID RNPL RANCA
AC P14626;
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3 DWLTFQKKHLTNTRDVDCNNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKNV 58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
01-APR-1990 (Rel. 14, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-FEB-1994 (Rel. 21, Last annotation update)
Ribonuclease, liver (EC 3.1.27.5).
Rana catesbelana (Bull frog).
Rukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia: Batrachia; Anura; Neobatrachia; Ranoidea; Rana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                J. Blochem. 106:729-735(1989).
-!- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-phosphates and 3'-phosphatoligonucleotides ending in C-P or U-P with 2', 3'-cyclic phosphate intermediates.
-!- SUBCELLULAR LOCATION: Secreted.
-!- SUBLEMILY: Belongs to the pancreatic ribonuclease family.
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Bukaryota, Metazoa; Chordata, Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Iguanidae; Iguaninae; Iguana.

NCBI_TaxID=8517;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   59 LITSEFYLSDC---NVTSRPCKYKLKKSTNIFCVICENQAPVHFVGVGHC 105
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"The amino acid sequence of iguana (Iguana iguana) pancreatic
ribonuclease.";
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1-FEB-1994 (Rel. 28, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Ribonuclease pancreatic (EC 3.1.27.5) (RNase 1) (RNase A).
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42.7%; Pred. No. 1.6e-21;
ive 19; Mismatches 37;
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                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=90130374; PubMed=2613682;
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MEDLINE=94139745; PubMed=8307028;
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HSSP; P11916; 1BC4.
InterPro; IPR001427; RNaseA.
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Best Local Similarity
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35
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P119f6, Q9PWR7;
01-QCT-1989 (Rel. 12, Created)
10-QCT-2003 (Rel. 42, Last sequence update)
10-QCT-2003 (Rel. 42, Last annotation update)
Ribonuclease, occytes precursor (BC 3.1.27.-) (RC-RNase) (Sialic acid-binding lectin) (SBL-C).
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                                                                                                                                                                                                                                                                                                                                                                                                                        DWLTFQKKHITNTRDVDCDNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTTS
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MEDLINE=87299649; PubMed=3304421;
Titani K., Takio K., Kuwada M., Nitta K., Sakakibara F., Kawauchi H.,
Titani K., Takio K., Kuwada M., Nitta K., Sakakibara F., Kawauchi H.,
Takayanagi G., Hakomori S.;
"Amino acid sequence of sialic acid binding lectin from frog (Rana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Liver;
MEDLINE=98165825; PubMed=9497370;
Huang H.C., Wang S.C., Leu Y.J., Lu S.C., Liao Y.D.;
Huang H.C., Wang S.C., ret Y.J., Lu S.C., Liao Y.D.;
The Rana catesbelana ror gene encoding a cytotoxic ribonuclease.
Tissue distribution, cloning, purification, cytotoxicity, and active residues for RNase activity.";
J. Biol. Chem. 273:6395-6401(1998).
                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rana catesbeiana (Bull frog).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Amphibia, Batrachia, Anura, Neobatrachia, Ranoidea, Ranidae, Rana
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                                                                                                                                                                                                                                                                                                                                     Score 551; DB 1; Length 104;
Pred. No. 3.9e-52;
                                                                                                                                                                                                                                                                                                                                                                       2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "A pyrimidine-guanine sequence-specific
catesbeiana (bullfrog) oocytes.";
Nucleic Acids Res. 20:1371-1377(1992).
[4]
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Liao Y.-D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       catesbeiana) eggs.";
Biochemistry 26:2189-2194(1987).
                                                                                                                                                                                                                                                                                                                                       94.78;
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 SEQUENCE OF 23-133.
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Best Local Similarity
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                MEDIANE=98437383; PubMed=9761686; Chan Y.-C., Chen Y.-C., Hom K., Huang R.-F., Huang T.H.; Chan C., Chen Y.-C., How K., Huang R.-F., Huang T.H.; The solution structure of a cytotoxic ribonuclease from the oocytes of Rana catesbeiana (bullfrog)."; J. Mol. Biol. 283:231-244(1998).

-!-FUNCTION: Preferentially cleaves single-stranded RNA at pyrimidine residues with a 3'flanking guanine. Hydrolyzes poly(U) and poly(C) as substrates, and prefers the former. The S-lectins in frog eggs may be involved in the fertilization and development of the frog embryo. This lectin agglutinates various animal cells, including normal lymphocytes, erythrocytes, and fibroblasts of animal and human origin. It is cytotoxic against several tumor cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART; SM0092; RNASE Pc; 1.
PROSITE; PS00127; RNASE PANCREATIC; 1.
Hydrolase; Nuclease; Endonuclease; Sialic acid; Lectin; 3D-structure;
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8
TISSUB-EGG;
MEDLINE=93192604; PubMed=8448385;
MEDLINE=93192604; PubMed=8448385;
Nitta K., Oyama F., Oyama R., Sekiguchi K., Kawauchi H.,
Takayanagi Y., Hakomori S., Titani K.;
"Ribonuclease activity of sialic acid-binding lectin from Rana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: Belongs to the pancreatic ribonuclease family.
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PYRROLIDONE CARBOXYLIC ACID.
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PDB; 1BC4; 28-OCT-98.
PDB; 1MO7; 21-JAN-03.
Interpro; IPR001427; RNaseA.
Pfam; PF00074; rnaseA; 1.
ProDom; PD000535; RNaseA; 1.
                                                                                                                                                        Glycobiology 3:37-45(1993).
                                                                                                                                                                                                             STRUCTURE BY NMR OF 23-133
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122
133 AA;
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SEQUENCE
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

7, 2004, 21:30:40; Search time 5.30402 Seconds (without alignments) 1030.796 Million cell updates/sec May Run on:

US-09-961-400-13 582 1 MSDWLTFQKKHLTNTRDVDC.....TFCVTCENQAPVHFVGVGHC 105 Title: Perfect score: Sequence:

Scoring table:

141681 segs, 52070155 residues BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched:

141681 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	P22069 rana pipien P11916 rana catesb P1883 rana catesb P80287 iguana igua P80287 iguana igua P80287 iguana igua P80287 iguana igua P80287 iguana igua P80287 iguana igua P80215 mus musculu P80676 myocastor C P80679 cavia porce P80679 cavia porce P80679 cavia porce P80679 cavia porce P80679 cavia porce P80679 cavia porce P80679 cavia porce P80679 cavia porce P80677 hydrochoeru P801570 mus musculu P80677 hydrochoeru P80677 hydrochoeru P80672 hippopotamu Q8wn65 miopithecus P80672 in ppopotamu Q8wn65 miopithecus P80673 usu sarcola P80671 sus sarcola P80671 sus sarcola P80671 sus sarcola P80674 equus cabal Q8wn60 sapien P80674 equus cabal Q8wn60 sapien P80674 equus cabal Q8wn60 sapien P80674 equus cabal
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ANGI PIG	RNPA_CAVPO	RNBR_GIRCA	ANGI SAGOE	RNBR AXIPR	ECP2 MOUSE	ANG2_BOVIN	RNP AEPME	RNP_ANTAM	RNP_SHEEP	RNS6_SAISC
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6. 6. 4. 7.	36	37	38	9	40	41	42	43	44	45

ALIGNMENTS

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                                                                                                                                                                          20; Gaps
                                                                                                               Query Match 20.1%; Score 117; DB 1; Length 128; Best Local Similarity 28.0%; Pred. No. 0.00011; Matches 33; Conservative 21; Mismatches 44; Indels
C;Keywords: hydrolase; nucleic acid digestion; pancreas F;12,41,119/Active site: His, Lys, His #status predicted F;26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted
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anglogenin - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Accession: S2983; B43825
C;Accession: S2983; B43825
B;Bond, M.D.; Strydom, D.J.; Vallee, B.L.
Biochim. Biophys. Acta 1162, 177-186, 1993
A;Title: Characterization and Sequencing of rabbit, pig and mouse angiogenins: discernme A;Reference number: S29833
A;Title: Characterization and Sequencing of Pabbit, pig and mouse angiogenins: discernme A;Reference number: S29833
A;Accession: 63 VPCKNGQTNCYQSYSSMHITDCRVTSNSKFPDCSYRTTQAQKSIVVACEGNLYVPVHF 120 g

Query Match

19.9%; Score 116; DB 1; Length 125;
Best Local Similarity 31.2%; Pred. No. 0.00013;
Matches 24; Conservative 13; Mismatches 32; Indels

31 CKDKNTFIYSRPEPVKAICK---GIIASKNV-LTTSEFYLSDCNVTS----RPCKYKLKK 82 Gaps .. 8

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83 STNTFCVTCENQAPVHF 99

99 GSRNIVIACENGLPVHF 115

Search completed: May 7, 2004, 21:54:54 Job time: 9.5276 secs

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C;Keywords: angiogenesis; hydrolase; nucleic acid degradation; pyroglutamic acid
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Superfamily: pancreatic ribonuclease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         R; van den Berg, A.; van den Hende-Timmer, L.; Hofsteenge, J.; Gaastra, W.; Beintema, J.J
Bur. J. Biochem. 75, 91-100, 1977
A;Title: Guinea pig pancreatic ribonucleases. Isolation, properties, primary structure a
A;Reference number: A91247; MUID:77185023; PMID:862624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Description: hydrolyzes tRNA; induces vascularization of normal and malignant tissues C; Superfamily: pancreatic ribonuclease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NyAlternate names: angiogenesis factor
NyAlternate names: angiogenesis factor
CySpecies: Mus musculus (Douse mouse)
CySpecies: Mus musculus (house mouse)
CyAccession: A35932
Ry Bond, M.D.; Vallee, B.L.
Biochem. Biophys. Res. Commun. 171, 988-955, 1990
A;Title: Isolation and sequencing of mouse angiogenin DNA.
A;Reference number: A35932; MuID:91025023; PMID:2222458
A;Accession: A35932
A;Status: not compared with conceptual translation
A;Reiden: DNA
A;Rescidues: 1-145 cBON>
A;Cross-references: GB:U22516; NID:9726325; PIDN:AAA91366.1; PID:g726326
C;Genetics:
A;Introns: #status absent
C;Function:
A;Description: bydrolyzes tRNA; induces vascularization of normal and malignant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28
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                                                                                                                                   63
                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Cavia porcellus (guinea pig)
C;Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 31-Mar-2000
C;Accession: A00826
                                                                                                                                                                                                          64 PCKNGQSNCYESTSNBMHITDCRLTSNSKFPDCLYRTSQEEKSIIVACEGNPYVPVHF 120
                                                                                                                                   8 PORQHIDSSGSPSTNPNYCNAMMKSRNMTQERCKPVNTFVHEPLADVQAVC----FQKNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | : || :: |: || SSAMKFQRQHMDPEGSPSNSSNY-CNVMMIRRNWIQGRCKPVNIFVHESLADVQAVC---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISEFYLSDCNVTSRP----CKYKLKKSTNTFCVTCENQ--AP
                                                                                        7 FQKKHL-----INTRDVDCNNIM-SINLF--HCKDKNTFIYSRPEPVKAICKGIIASKNV
                                                                                                                                                                                  99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 SDWLTFQKKHL-----TNTRDVDCNNIM---STNLFHCKDKNTFIYSRPEPVKAICKGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                  Gaps
                                                                                                                                                                                                                                                                                                                                             B - guinea pig (tentative sequence)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Note: 64-Pro was also found
C;Superfamily: pancreatic ribonuclease
C;Keywords: glycoprotein, hydrolase; nucleic acid digestion; pancreas
C;Keywords: glycoprotein, hydrolase; nucleic acid digestion; pancreas
F;12,41,119/Active site: His Lys, His #status predicted
F;21,34/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted
                                                                                                                                                                                  -LITSEFYLSDCNVTSR----PCKYKLKKSTNTFCVTCENQ--APVHF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30;
                                               28;
    Length 128;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5.3e-05;
ches 37;
20.6%; Score 120; DB 1; 29.9%; Pred. No. 5.3e-05; iive 18; Mismatches 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20.6%; Score 120; DB 1;
28.5%; Pred. No. 5.3e-05;
ive 21; Mismatches 37.
                                                                                                                                                                                                                                                                                                                                           pancreatic ribonuclease (EC 3.1.27.5) N/Alternate names: RNase IB
                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: protein A; Residues: 1-128 < VAN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 35; Conserv
                     Best Local Similarity
Matches 35; Conser
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  Query Match
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Fil-24/Domain: signal sequence #status predicted <SIG>
Fi2-145/Product: angiogenin #status predicted <MAT>
Fi25-145/Product: angiogenin #status predicted <MAT>
Fi25/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted
Fi37,64,137/Active site: His, Lys, His #status predicted
F:50-104,63-115,81-130/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         guinea-pig: comparison of the amir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;van den Berg, A.; van den Hende-Timmer, L.; Beintema, J.J.
alochim. Blochim. 453, 400-469, 1976
A;Title: Isolation, properties and primary structure of coypu and chinchilla pancreatic A;Reference number: A90612; MUID:77065676; PMID:999896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pancreatic ribonuclease (EC 3.1.27.5) - Chinchilla brevicaudata (tentative sequence) NiAlternate names: RNase 1, RNase A C;Species: Chinchilla brevicaudata, Chinchilla lanigera brevicaudata Cipate: 24-Apr-1984 #sequence_revision 30-Sep-1988 #text_change 31-Mar-2000 C;Accession: A00820
                                                                                                                                                                                                                                                                                                     5,
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NyAlternate names: RNase 1; RNase A
Cyppecies: Hydrochaeris hydrochaeris (capybara, carpincho)
Cypacies: 103-Aug-1984 #sequence_revision 03-Aug-1984 #text_change 29-Oct-1999
CyAccession: A00824
RyBeintema, J.J.; Neuteboom, B.
RyBeintema, J.J.; Neuteboom, B.
A. Mol. Evol. 19, 145-152, 1983
A/Title: Origin of the duplicated ribonuclease gene in guinea-pig: comparisc A, Reference number: A92957; MUID:87036770; PMID:6571219
                                                                                                                                                                                                                                                                                                                                                                                                                                              32 KFLTQHHDAKPKGRDDRYCERMMKRRSLTSPCKDVNTFIHGNKSNIKAICGANGSPYREN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 SSAMKFQRQHMDSSGSPSTINANYCNEMMKGRNMTQGYCKPVNTFVHEPLADVQAVC----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --LTTSEFYLSDCNVTSRP----CKYKLKKSTNTFCVTCENQ--APV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59 FQKNVPCKNGQSNCYQSNSNMHITDCRLTSNSKYPNCSYRTSRENKGIIVACEGNPYVPV
                                                                                                                                                                                                                                                                                                                                                                              -CNNIMSTNLF--HCKDKNTFIYSRPEPVKAIC--KGIIASKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 SDWLTFQKKHL----TNTRDVDCNNIM---STNLFHCKDKNTFIYSRPEPVKAICKGII
                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C, Superfamily: pancreatic ribonuclease
C; Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F;12,41,119/Active site: His, Lys, His #status predicted
F;26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted
F;34/Binding site: carbohydrate (Asn) (covalent) #status experimental
                                                                                                                                                                                                                                                                                                     17;
                                                                                                                                                                                                                             DB 1; Length 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               138
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A;Note: a second component of chinchilla ribonuclease has 32-Asp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58 V-LITSEFYLSDCNVTS----RPCKYKLKKSTNTFCVTCENQAPVHF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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                                                                                                                                                                                                                             20.5%; Score 119.5; DB 1
30.8%; Pred. No. 6.8e-05;
iive 12; Mismatches 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20.3%; Score 118; DB 1; 27.0%; Pred. No. 8.2e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19; Mismatches
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7;

Gaps

28;

28 63

99

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C,Accession: A00818
R,Emmens, M.; Welling, G.W.; Beintema, J.J.
Bicchem. J. 157, 317-323, 1976
A;Title: The amino acid sequence of pike whale (lesser rorqual) pancreatic ribonuclease A;Reference number: A00818
A;Accession: A00818
A;Accession: A00818
A;Molecule type: protein
A;Residues: 1-124 <a href="https://www.molecule-cype:-protein">molecule-cype:-protein</a>
C;Superfamily: pancreatic ribonuclease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Keywords: 91yCoprotein; hydrolase, nucleic acid digestion; pancreas F;12,41,119/Active site: His, Lys, His #status predicted F;26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted F;76/Binding site: carbohydrate (Asn) (covalent) (partial) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 LTFQKKHLTNTRDVD-----CNNIMSTNLF---HCKDKNTFIYSRPEPVKAICKGIIASK 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pancreatic ribonuclease (EC 3.1.27.5) - minke whale NiAlternate names: RNAse 1; RNase 1; C.Species: Balaenoptera acutoroostrata (minke whale, lesser rorgual) C.Species: Balaenoptera acutoroostrata (minke whale, lesser rorgual) C.Pate: 24-Apr_1984 #sequence_revision 24-Apr-1984 #text_change 03-Jun-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64 LCKNGQINCYQSNSNMHITDCRVTSNSDYPNCSYRTSQEEKSIVVACEGNPYVPVF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                  7 FQKKHL-----TNTRDVDCNNIM-STNLF--HCKDKNTFIYSRPEPVKAICKGIIASKNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8 FEROHMDSRGSPSTNPNYCNEMMKSRNMTQGRCKPVNTFVHEPLADVQAVC----FQKNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 MKFQRQHMDSGNSPGNNPNYCNQMMMRRKMTQGRCKPVNTFVHESLEDVKAVC----SQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57 NVL------TISEFYLSDCNVTSRP----CKYKLKKSINTFCVTCENQ--APVHF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -TISEFYLSDCNVTSRP----CKYKLKKSINIFCVTCENQ--APVHF
                                           C;Superfamily: pancreatic ribonuclease
C;Keywords: glycoprotein, hydrolase, nucleic acid digestion, pancreas
F;12.41,119/Active site: His, Lys, His #status predicted
F;26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted
                                                                                                                                                       F;26-84,40-95,58-110,65-72/Disulfide Dollus: #Status processive F;34/Binding site: carbohydrate (Asn) (covalent) #status experimental
                                                                                                                                                                                                                                                                               Length 128;
                                                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                           Query Match 21.6%; Score 126; DB 1; L. Best Local Similarity 29.9%; Pred. No. 1.3e-05; Matches 35; Conservative 18; Mismatches 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21.5%; Score 125; DB 1; 28.6%; Pred. No. 1.6e-05;
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Best Local Similarity
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Matches
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R/Acharya, K.R.; Shapiro, R.; Riordan, J.F.; Vallee, B.L.
Proc. Natl. Acad. Sci. US.A. 92, 2949-2953, 1995
Proc. Natl. Acad. Sci. US.A. 92, 2949-2953, 1995
A/Title: Crystal structure of bovine angiogenin at 1.5 Angstroms resolution.
A/Reference number: A58315; MUID:95224057; PMID:7708754
A/Contents: annotation; X-ray crystallography, 1.5 angstroms
R/Lequin, O.; Albaret, C.; Bontems, F.; Spik, G.; Lallemand, J.Y.
A/Contents: annotation; conformation by (1)H-NMR, residues 1-125
R/Lequin, O.; Albaret, C.; Bontems, F.; Spik, G.; Lallemand, J.Y.
Blochemistry 35, 8870-8880, 1996
A/Title: Solution structure of bovine angiogenin by (1)H nuclear magnetic resonance spec
A/Reference number: A58921; MUID:96280645; PMID:8688423
A/Contents: annotation; conformation by (1)H-NMR
R/Reference number: A58921; MUID:96280645; PMID:8688423
A/Contents: annotation; conformation by (1)H-NMR
R/Reference number: A58921; MUID:96280645; PMID:8680423
A/Contents: annotation; conformation by (1)H-NMR
R/Reference number: A58921; MUID:96280645; PMID:8680423
A/Contents: annotation; Conformation by (1)H-NMR
R/Reference number: A58921; MUID:96280645; PMID:86280645; PMID:862806465; PMID:862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (1)H nuclear magnetic resonance sped
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A, Description: hydrolyzes tRNA; induces vascularization of normal and malignant tissues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A, Title: Isolation, properties and primary structure of coypu and chinchilla pancreatic A, Reference number: A90612, MUID: 77065676; PMID: 999896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ġ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24 DEYCENMMKNRRITRPCKDRNTFIHGNKNDIKAICE----DRNGQPYRGDLRISKSEFQI 79
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C;Date: 24-Apr-1984 #sequence_revision 30-Sep-1988 #text_change 31-Mar-2000
C;Accession: A00822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                       C.; Montreuil, J.; Spik, G.; Tartar,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18;
                                                                                                                                                                                                                                                               A.Experimental source: plasma
R.Maes, P.; Damart, D.; Rommens, C.; Montreuil, J.; Spik, G.; Tartar
FEBS Lett. 241, 41-45, 1988
A.Fitle: The complete amino acid sequence of bovine milk angiogenin.
A.Reference number: S02001; MUID:89065101; PMID:3197838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pancreatic ribonuclease (EC 3.1.27.5) - nutria (tentative sequence)
N;Alternate names: RNase 1; RNase A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22.0%; Score 128; DB 1; Length 125; 34.0%; Pred. No. 8.2e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32; Indels
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C)Keywords: anglogenesis; hydrolase; nucleic acid degradation
E;60-68/Region: receptor hydrolase; status predicted
F;14,41,115/Active site: His, Lys, His #status predicted
F;27-82,40-93,58-108/Disulfide bonds: #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Experimental source: milk R; Riordan, J.F.; Vallee, B.L. R;Acharya, K.R.; Shapiro, R.; Riordan, J.F.; Vallee, B.L. submitted to the Brookhaven Protein Data Bank, January 1995 A; Reference number: A65065; PDB:1AGI
                                                                           A, Title: Amino acid sequence of bovine angiogenin. A, Reference number: A32474; MUID:89375344; PMID:2775757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Reference number: S48212; MUID:95010071; PMID:7925406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R; van den Berg, A.; van den Hende-Timmer, L.; Beintema, Biochim. Biophys. Acta 453, 400-409, 1976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Contents: annotation; conformation by (1) H-NMR C; Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14; Mismatches
Bond, M.D.; Strydom, D.J.
lochemistry 28, 6110-6113, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 34.08
Matches 33; Conservative
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A,Accession: A00822
A,Molecule type: protein
                                                                                                                                                                                           A;Molecule type: protein A;Residues: 1-125 <BON>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Residues: 1-125 < MAE>
                                                                                                                                                       ;Accession: A32474
                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Accession: S02001
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Gaps

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Indels

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Pancreatic ribonuclease (EC 3.1.27.5) - cuis
NyAlternate names: RNase 1; RNase A
C;Species: Galea mustabloides (cuis)
C;Date: 03-Aug-1984 #sequence_revision 03-Aug-1984 #text_change 04-Oct-1996
C;Accession: A00827
R;Beintema, J.J.; Neuteboom, B.
J. Mol. Evol. 19, 145-152, 1983
J;Title: Origin of the duplicated ribonuclease gene in guinea-pig: comparison of the amir A;Reference number: A92957; MUID:87036770; PMID:6571219
A;Reference number: A92957; MUID:87036770; PMID:6571219
A;Residues: 1-124 - 6BEI>
A;Residues: 1-124 - 6BEI>
A;Residues: 1-124 - 6BEI>
A;Residues: 1-124 - 6BEI>
C;Comment: The cuis is a rodent belonging to the same subfamily as the guinea pig. C;Comment: The cuis is a rodent belonging to the same subfamily as the guinea pig. C;Comment: The cuis is a rodent belonging to the same subfamily as the guinea pig. C;Comment: The cuis is a rodent belonging to the same subfamily as F;12,41,119/Active site: His Iys, His #status predicted
F;26-64,40-95,58-110,65-72/pisulfide bonds: #status predicted
F;26-64,40-95,58-110,65-72/pisulfide bonds: #status predicted
F;94/Binding site: carbohydrate (Asn) (covalent) #status absent
C;Species: Iguana iguana (common iguana)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 21-Aug-1998
C;Accession: S41111
R;Zhao, W; Beintema, J.J.; Hofsteenge, J.
Bir. J. Bicchem. 219, 641-646, 1994
A;Title: The amino acid sequence of iguana (Iguana iguana) pancreatic ribonuclease.
A;Reference number: S41111; MUID:94139745; PMID:8307028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Angiogenin [validated] - bovine
NyAlternate names: angiogenesis factor
NyContains: ribonuclease (EC 3.1.27.
C)Species: Bos primigenius turus (cattle)
C,Date: 25-Sep-1989 #sequence revision 25-Sep-1989 #text_change 15-Sep-2000
C,Accession: A32474; S02001; A30044; S48212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59 -- SQKNVPCKNGQTNCYQSHSSMRITDCRVTSSSKYPNCSYRMIQAQKSIIVACEGTPSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 DWLTFQKKHL-----TNTRDVDCNNIM---STNLFHCKDKNTFIYSRPEPVKAIC--KG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 SDWLTFQKKHL-----TNTRDVDCNNIM---STNLFHCKDKNTFIYSRPEFVKAICKG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 THYEDNLYDSNESFDLTDCKNVGGTAPSSCKYNGTPGTKRIRIACENNQPVHF 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                52 IIASKNVLTTSE-FYLSDC----NVTSRPCKYKLKKSTNTFCVTCENQAPVHF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24.7%; Score 144; DB 2; 30.1%; Pred. No. 1.9e-07; ive 19; Mismatches 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22.7%; Score 132; DB 1; 30.6%; Pred. No. 3.2e-06; iive 18; Mismatches 36
                                                                                                                                                                                                                                                                                                                                                          A,Molecule type: protein
A,Residues: 1-119 <ZHA>
C,Superfamily: pancreatic ribonuclease
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Conservative 18;
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34; Conservative 1
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Les 38; Conserv
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                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary
                                                                                                                                                                                                                                                                                     A; Accession: S41111
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C;Species: Rana catesbeiana (bullfrog)
C;Species: Rana catesbeiana (bullfrog)
C;Species: Rana catesbeiana (bullfrog)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 05-Aug-1994
C;Accession: JX0085
R;Nitta, R.; Katayama, N.; Okabe, Y.; Iwama, M.; Watanabe, H.; Abe, Y.; Okazaki, T.; Ohg
J; Biochem. 106, 729-735, 1989
A;Title: Primary structure of a ribonuclease from bullfrog (Rana catesbeiana) liver.
A;Reference number: JX0085
A;Accession:                                                                                                                                                                                                                                                                                                              ribonuclease-related stalic acid-binding lectin - Japanese frog C;Species: Rana japonica (Japanese frog) C;Species: Rana japonica (Japanese frog) C;Accession: Juo.Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999 C;Accession: JX0120 R;Kamiya, Y.; Oyama, F.; Oyama, R.; Sakakibara, F.; Nitta, K.; Kawauchi, H.; Takayanagi, J. Biochem. 108, 139-143, 1990 A;Title: Amino acid sequence of a lectin from Japanese frog (Rana japonica) eggs. A;Reference number: JX0120, MUID:91035319; PMID:2229005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2;
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                                                        LITSEFYLSDC---NVTSRPCKYKLKKSTNIFCVICENQAPVHFVGVGHC 105
                                                                                                                        LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Experimental source: egg
C;Superfamily: pancreatic ribonuclease
C;Keywords: lectin; pyroglutamic acid
F;I/Modified site: pyroglone carboxylic acid (Gln) #status exp
F;19-72,34-82,52-97,94-111/Disulfide bonds: #status experimental
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48.2%; Score 280.5; DB 1;
Best Local Similarity 44.5%; Pred. No. 3.6e-21;
Matches 49; Conservative 19; Mismatches 35;
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Indels

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GenCore version 5.1.6
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OM protein - protein search, using sw model

7, 2004, 21:38:36; Search time 9.5276 Seconds (without alignments) 1060.090 Million cell updates/sec May Run on:

US-09-961-400-13 582 1 MSDWLTFQKKHLTNTRDVDC.....TFCVTCENQAPVHFVGVGHC 105 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 segs, 96191526 residues Searched:

283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	ribonuclease-relat	b	ribonuclease-relat	pancreatic ribonuc				pancreatic ribonuc	pancreatic ribonuc	pancreatic ribonuc	pancreatic ribonuc	-			angiogenin - rabbi	pancreatic ribonuc			pancreatic ribonuc	pancreatic ribonuc	pancreatic ribonuc	ribonuclease 4 (EC	ribonuclease - dom	pancreatic ribonuc	pancreatic-type ri	angiogenin - pig	ë	pancreatic ribonuc	
SUMMARIES	CT CT	iö	A27121	JX0120	JX0085	841111	NRUI	A32474	NRCU	NRWHK	NRKS	NRGPB	A35932	NRCB	NRYY	B43825	NRHP	NRHUAG	NRBOB	NRPG	NRPQ	NRBO	I52489	S08549	NRHO	S20066	A43825	JC6159	NRGPA	JC6160
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ah	Query Match	94.7	49.3	48.2	45.4	24.7	22.7	22.0	21.6	21.5	20.6	20.6	20.5	20.3	20.1	19.9	19.6	19.4	19.2	19.2	19.2	19.2	19.2	19.1	19.1	19.1	19.0	19.0		
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ALIGNMENTS

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Search completed: May 7, 2004, 21:51:57 Job time: 33.6904 secs

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; Sequence 8, Application US/09948391A; Publication No. US20030027311A1; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Rana pipiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 104
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Best Local S
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                                                                                                                                                                                                                                                                                             Length 104;
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                                                                                                                                                                                                                                                                                                                                   1; Indels
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APPLICANT: Newton, Dianne L.
APPLICANT: Newton, Dianne L.
APPLICANT: The United States of America
APPLICANT: The United States of America
APPLICANT: as represented by The Secretary of the
APPLICANT: Department of Health and Human Services
ITILE OF INVENTION: Recombinant Anti-Tumor RNase
FILE REPRENCE: 015280-343110US
CURRENT APPLICATION NUMBER: US/09/948,391A
CURRENT FILING DATE: 1998-03-27
PRIOR FILING DATE: 1998-03-27
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 1090-08-17
NUMBER OF SEQ ID NOS: 43
                                                                                                                                                                                                                                                                                      96.9%; Score 564; DB 10;
99.0%; Pred. No. 4.4e-57;
live 0; Mismatches 1;
                                                                                                                                                                                                                      ; OTHER INFORMATION: ribonuclease (RaPLR1)
US-09-948-391A-2
PRIOR FILING DATE: 1999-03-26
PRIOR APPLICATION NUMBER: US 09/622,613
PRIOR FILING DATE: 2000-08-17
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4, Application US/09948391A Publication No. US20030027311A1 GENERAL INFORMATION:
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Best Local Similarity 99.0%
Matches 102; Conservative
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Best Local Similarity
Matches 101; Conserv
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                                                                                                            SEQ ID NO 2
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RESULT 14 US-09-961-400-4

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Sequence 4, Application US/09961400

GENERAL INFORMATION:
APPLICANT: RYBAK, SUSANNA M.
APPLICANT: RYBAK, SUSANNA M.
APPLICANT: GOLDENBERG, DAVID M.
APPLICANT: GOLDENBERG, DAVID M.
TITLE OF INVENTION: LELLS
TITLE OF INVENTION: CELLS
TITLE OF INVENTION: CELLS
TITLE OF INVENTION: CELLS
CURRENT APPLICATION NUMBER: US/09/961,400
CURRENT APPLICATION NUMBER: US/09/25
FILE REPERENCE: 2001-09-25
PRIOR APPLICATION NUMBER: PCT/US99/06641
PRIOR APPLICATION NUMBER: PCT/US99/06641
PRIOR APPLICATION NUMBER: PCT/US99/06641
PRIOR PILING DATE: 1999-03-26
PRIOR PILING DATE: 1999-03-26
PRIOR PILING DATE: 1998-03-26
PRIOR FILING DATE: 1998-03-26
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APPLICANT: Newton, Dianne L.
APPLICANT: The United States of America
APPLICANT: The United States of America
APPLICANT: as represented by The Secretary of the
APPLICANT: as represented by The Secretary of the
TITLE OF INVENTION: Recombinant Anti-Tumor RNase
FILE REFERENCE: 015280-343110US
CURRENT APPLICATION NUMBER: US/09/948,391A
CURRENT FILING DATE: 1998-03-10
PRIOR FILING DATE: 1998-03-26
PRIOR FILING DATE: 1998-03-26
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 1099-03-26
PRIOR FILING DATE: 2000-08-17
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PATCHTIN UNER: 2.0
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; ORGANISM: Rana pipiens
US-09-961-400-28
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US-09-948-391A-2
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US-09-961-400-8
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APPLICANT: GOLDENBERG, DAVID M.
APPLICANT: GOLDENBERG, DAVID M.
APPLICANT: GOLDENBERG, DAVID M.
TATLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
TITLE OF INVENTION: CELLS
FILE REPRENCE: 018733/1059
CURRENT FILING DATE: 2001-09-25
FILE REPRENCE: 018733/1059
CURRENT FILING DATE: 2000-08-17
FRIOR APPLICATION NUMBER: 09/622,613
FRIOR FILING DATE: 1999-03-26
FRIOR FILING DATE: 1999-03-26
FRIOR FILING DATE: 1999-03-26
NUMBER OF SEQ ID NOS: 43
SORTWARE: Patentin Ver. 2.1
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  63 BEYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
                                  EFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
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                                                                                                                                                                                                                                                            JOHNSTON INFORMATION:

APPLICANT: Newton, Dianne L.

APPLICANT: Newton, Dianne L.

APPLICANT: The United States of America
APPLICANT: The United States of America
APPLICANT: The United States of America
APPLICANT: Benefit as represented by The Secretary of the
APPLICANT: Department of Health and Human Services
ITILE OF INVENTION: Recombinant Anti-Tumor RNase
FILE REFERENCE: 015280-3431100S
CURRENT APPLICATION NUMBER: US/09/948,391A
CURRENT FILING DATE: 1998-00-27
PRIOR FILING DATE: 1998-00-26
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 2000-08-17

PRIOR FILING DATE: 2000-08-17

SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                       Sequence 28, Application US/09948391A
Publication No. US20030027311A1
GENERAL INFORMATION:
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ORGANISM: Rana pipiens
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US-09-961-400-28
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APPLICANT: RYBAK, SUSANNA M.
APPLICANT: RYBAK, SUSANNA M.
APPLICANT: RYBAK, DAVID M.
APPLICANT: GOLDENBERG, DAVID M.
APPLICANT: MEWTON, DIANNE L.
TITLE OF INVENTION: CELLS
TITLE OF INVENTION: CELLS
TITLE OF INVENTION: CELLS
TITLE OF INVENTION: 108733/1059
CURRENT APPLICATION NUMBER: 09/622,613
PRIOR PAPLICATION NUMBER: 09/622,613
PRIOR PAPLICATION NUMBER: PCT/US99/06641
PRIOR PILING DATE: 1999-03-26
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 1999-03-26
NUMBER OF SEQ ID NOS: 43
SSEY ID NO 88
SSEY ID NO 88
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                                                                                                                                  3 DWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTTS
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                 Length 127;
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                                                                        0; Indels
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APPLICANT: Newton, Diame L.
APPLICANT: The United States of America
APPLICANT: as represented by The Secretary of the
APPLICANT: Department of Health and Human Services
TITLE OF INVENTION: Recombinant Anti-Tumor RNase
FILE REFERENCE: 015280-343110US
                    Score 573; DB 10;
Pred. No. 5.1e-58;
98.5%; Scc...
100.0%; Pred. No. ...
'... 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 8, Application US/09961400; Publication No. US20030124131A1; GENERAL INFORMATION:
                 Query Match
Best Local Similarity 100.
Matches 103; Conservative
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ORGANISM: Rana pipiens
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WESOLI 6

Sequence 2, Application US/09961400

Sequence 2, Application No/09961400

PUBLication No. US20030124131A1

GENERAL INFORMATION:

APPLICANT: RYBAK, SUSANNA M.

APPLICANT: ROLDENBERG, DAVID M.

APPLICANT: NEWTON, DIANNE L.

TITLE OF INVENTION: CELLS

FILE REPERENCE: 018733/1059

CURRENT APPLICATION NUMBER: US/09/961,400

CURRENT PILING DATE: 2001-09-25

PRICR FILING DATE: 2000-08-17

PRICR FILING DATE: 1999-03-26

PRICR FILING DATE: 1999-03-26

PRICR FILING DATE: 1999-03-26

PRICR FILING DATE: 1998-03-26

PRICR PRILING DATE: 1998-03-26

PRICR PRILING DATE: DATE NUMBER: PUBLICATION NUMBER: PUBLICATION NUMBER: PUBLICATION NUMBER: PUBLICATION NUMBER: PUBLICATION NUMBER: PUBLICATION NUMBER: PUBLICATION NUMBER: PUBLICATION NUMBER: PUBLICATION NUMBER: PUBLICATION NUMBER: PUBLICATION NUMBER: PUBLICATION NUMBER: PUBLICATION NUMBER: PUBLICATION NUMBER: PUBLICATION NUMBER: PUBLICATION NUMBER: PUBLICATION NUMBER: PUBLICATION NUMBER: PUBLICATION NUMBER: PUBLICATION NUMBER: PUBLICATION NUMBER: PUBLICATION NUMBER: PUBLICATION NUMBER: PUBLICATION NUMBER: PUBLICATION NUMBER: PUBLICATION NUMBER: PUBLICATION NUMBER: PUBLICATION NUMBER: PUBLICATION NUMBER: PUBLICATION NUMBER: PUBLICATION NUMBER: PUBLICATION NUMBER: PUBLICATION NUMBER: PUBLICATION NUMBER: PUBLICATION NUMBER: PUBLICATION NUMBER: PUBLICATION NUMBER: PUBLICATION NUMBER: PUBLICATION NUMBER: PUBLICATION NUMBER: PUBLICATION NUMBER: PUBLICATION NUMBER: PUBLICATION NUMBER: PUBLICATION NUMBER: PUBLICATION NUMBER: PUBLICATION NUMBER: PUBLICATION NUMBER: PUBLICATION NUMBER: PUBLICATION NUMBER: PUBLICATION NUMBER: PUBLICATION NUMBER: PUBLICATION NUMBER: PUBLICATION NUMBER: PUBLICATION NUMBER: PUBLICATION NUMBER: PUBLICATION NUMBER: PUBLICATION NUMBER: PUBLICATION NUMBER: PUBLICATION NUMBER: PUBLICATION NUMBER: PUBLICATION NUMBER: PUBLICATION NUMBER: PUBLICATION NUMBER: PUBLICATION NUMBER: PUBLICATION NUMBER: PUBLICA
                                                                                                              APPLICANT: RYBAK, SUSANNA M.
APPLICANT: RYBAK, SUSANNA M.
APPLICANT: GOLDENBERG, DAVID M.
FAPLICANT: GOLDENBERG, DAVID M.
TITLE OF INVENTION: INMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
TITLE OF INVENTION: CELLS
FILE REFERENCE: 01873/1059
CURRENT APPLICATION NUMBER: US/09/961,400
CURRENT APPLICATION NUMBER: 09/622,613
PRIOR APPLICATION NUMBER: 09/622,613
PRIOR APPLICATION NUMBER: 09/6241
PRIOR APPLICATION NUMBER: 60/079,751
PRIOR PILING DATE: 1999-03-26
PRIOR FILING DATE: 1999-03-26
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PATENTIN USE: 2.1
SEQ ID NO 9
TEMPORE TO 11
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Pred. No. 2.6e-58;
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                            Sequence 9, Application US/09961400
                                                     Publication No. US20030124131A1
GENERAL INFORMATION:
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Best Local Similarity 98.1%;
Matches 103; Conservative
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; ORGANISM: Rana pipiens
US-09-961-400-2
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Best Local Similarity
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Best Local Similarity
Matches 103; Conserv
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Publication No. US20030124131A1

GENERAL INPORMATION:

APPLICANT: RYBAK, SUSANNA M.

APPLICANT: RYBATON:

TITLE OF INVENTION: DIANNE L.

TITLE OF INVENTION: CELLS

FILE REFERENCE: 019733/1059

CURRENT APPLICATION NUMBER: 09/622,613

FRICE RILING DATE: 2001-09-25

PRIOR APPLICATION NUMBER: PCT/US99/06641

FRICE RILING DATE: 1999-03-26

PRIOR FILING DATE: 1999-03-26

NUMBER OF SEQ ID NOS: 43

NUMBER OF SEQ ID NOS: 43

SOFFWARE: PATENTIN VET. 2.1
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CTHER INFORMATION: Description of Artificial Sequence:Rana pipiens
OTHER INFORMATION: ribonuclease with Gln1Ser substitution
CTHER INFORMATION: (recombinant RapLR1 Q1S)
US-09-948-391A-11
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99.1%; Score 577; DB 10; Length 104;
Best Local Similarity 100.0%; Pred. No. 1.4e-58;
Matches 104; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
99.1%; Score 577; DB 10;
Best Local Similarity 100.0%; Pred. No. 1.4e-58;
Matches 104; Conservative 0; Mismatches 0;
PRIOR APPLICATION NUMBER: US 60/079,751
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: WO PCT/US99/06641
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 2000-08-17
NUMBER OF SEQ ID NOS: 43
NUMBER OF SEQ ID NOS: 43
SOFFWARE: Patentin Ver. 2.0
SEQ ID NO 11
LENGTH: 104
                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Artificial Sequence
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ORGANISM: Rana pipiens
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US-09-961-400-11
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RESULT 7 US-09-961-400-9

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RESULT 5
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APPLICANT: GOLDENBERG, DAVID M.
APPLICANT: GOLDENBERG, DAVID M.
APPLICANT: GOLDENBERG, DAVID M.
TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
TITLE OF INVENTION: CELLS
TITLE OF INVENTION: CELLS
FILE REFREENCE: 108793/1059
CURRENT APPLICATION NUMBER: US/09/961,400
CURRENT FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: 09/622,613
PRIOR APPLICATION NUMBER: 09/622,613
PRIOR APPLICATION NUMBER: 60/079,751
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 1999-03-26
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PALCHING UNC: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
1 MSDWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLT 60
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                                                                               TSEFYLSDCNVTSRPCKYXLKKSTNTFCVTCENQAPVHFVGVGHC 105
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APPLICANT: The United States of America
APPLICANT: as represented by The Secretary of the
APPLICANT: Department of Health and Human Services
TITLE OF INVENTION: Recombinant Anti-Tumor RNase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: 015280-343110US
CURRENT APPLICATION NUMBER: US/09/948,391A
CURRENT APPLICATION NUMBER: US/09/948,391A
CURRENT FILING DATE: 2002-05-10
PRIOR FILING DATE: 1998-03-27
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 2000-08-17
NUMBER: OF SEQ ID NOS: 43
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 6, Application US/09948391A Publication No. US20030027311A1
                                                                                                                                                                                                    US-09-961-400-13
; Sequence 13, Application US/09961400
; Publication No. US20030124131A1
; GENERAL INFORMATION:
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Matches 105; Conservative
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ORGANISM: Rana pipiens
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LENGTH: 105
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APPLICANT: MICHARMALION;
APPLICANT: GOLDENBERG, DAVID M.
APPLICANT: GOLDENBERG, DAVID M.
TAPLICANT: GOLDENBERG, DAVID M.
TITLE OF INVENTION: IMMINOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
TITLE OF INVENTION: CELLS
TITLE OF INVENTION: CELLS
TITLE OF INVENTION: USUBJACOS
CURRENT APPLICATION NUMBER: 09/622,613
FRIOR PEPINGE TILING DATE: 2000-08-17
PRIOR PELLOR DATE: 2000-08-17
PRIOR PELLOR DATE: 1999-03-26
PRIOR APPLICATION NUMBER: 60/079,751
PRIOR APPLICATION NUMBER: 60/079,751
PRIOR APPLICATION NUMBER: 60/079,751
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                                                                                                                                                                                                                                                                                                             1 MSDWLIFOKKHLINTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLT
OTHER INFORMATION: Description of Artificial Sequence:Rana pipiens OTHER INFORMATION: ribonuclease with Met at position 1 (recombinant OTHER INFORMATION: Met(-1) RaPLR1)
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                                                                                                                                                                          Length 105;
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APPLICANT: The United States of America
APPLICANT: The United States of America
APPLICANT: as represented by The Secretary of the
APPLICANT: Department of Health and Human Services
TILLE OF INTWITION: Recombinant Anti-Tumor RNase
TILLE REPERBUCE: 015280-34111005
CURRENT APPLICATION NUMBER: US/09/948,391A
                                                                                                                                                                          99.3%; Score 578; DB 10;
99.0%; Pred. No. 1.1e-58;
iive 0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 6, Application US/09961400
; Publication No. US20030124131A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                             Best Local Similarity 99.0
Matches 104; Conservative
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ORGANISM: Rana pipiens
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GenCore version 5.1.6
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OM protein - protein search, using sw model

7, 2004, 21:29:40; Search time 33.6904 Seconds (without alignments) 865.070 Million cell updates/sec Мау Run on:

US-09-961-400-13 582 1 MSDWLTFQKKHLTNTRDVDC.....TFCVTCENQAPVHFVGVGHC 105

Perfect score: Seguence:

1140673 segs, 277566755 residues Gapop 10.0 , Gapext 0.5 Searched:

BLOSUM62

Scoring table:

Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Listing first 45 summaries Maximum Match 100% Post-processing: Minimum Match 0%

Database

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" (gnz 6/ptodata/2/pubpaa/US07 NEW PUB.pep:*
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Published_Applications_AA:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 13. Appl	7			7	11,	6	Sequence 2. Appli	28,	28,	8	. ~	Segmence 4. Appli	4	8
ID	US-09-948-391A-13	US-09-961-400-13	US-09-948-391A-6	US-09-961-400-6	US-09-948-391A-11	US-09-961-400-11	US-09-961-400-9	US-09-961-400-2	US-09-948-391A-28	US-09-961-400-28	US-09-961-400-8	US-09-948-391A-2	US-09-948-391A-4	US~09-961-400-4	US-09-948-391A-8
	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10
% Query Match Length DB	105	105	105	105	104	104	111	104	127	127	105	104	104	104	105
% Query Match	100.0	100.0	99.3	99.3	99.1	99.1	98.8	98.5	98.5	98.5	97.1	6.96	6.96	6.96	96.2
Score	582	582	578	578	577	577	575	573	573	573	565	564	564	564	260
Result No.	7	7	m	4	ഹ	9	7	80	6	10	11	12	13	14	15

Sequence 9, Appli Sequence 2, Appli Sequence 1, Appli Sequence 1, Appli	Sequence 35, Appl Sequence 3, Appli Sequence 3, Appli Sequence 26, Appl Sequence 26, Appl	10000	Sequence 21, Appl Sequence 22, Appl Sequence 22, Appl Sequence 15, Appl Sequence 15, Appl Sequence 17, Appl	9,99,199,199	Sequence 5, Appl. Sequence 103, App Sequence 6, Appl. Sequence 2, Appl. Sequence 254, App Sequence 254, App
-391A- -882-2 119-1 -887-1	-60-SD	10 US-09-961-400-17 10 US-09-948-391A-24 10 US-09-961-400-24 10 US-09-948-391A-21 10 US-09-671-400-21	0-80 0-80 0-80 0-80 0-80	US-09 US-09 US-10 US-10	12 US-10-030-447-15 12 US-10-037-417-103 9 US-09-286-240-6 9 US-09-863-777-2 9 US-09-731-872-254 10 US-09-876-997-254
111 105 104 104	83 83 111 111	1110011	117 117 110 110	110 110 119	124 124 147 147 147
96.2	76.5 76.5 49.1 49.1	48.4 48.2 4.7.7 7.7.7	7.74 4.7.74 7.74 2.74 3.74	246.8 455.8 27.1 7.44.7	221 221 231 24.4.60 24.4.4.4.4.4.4.4.4.4.4.4.4.4.4.4.4.4.4.
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ALIGNMENTS

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OTHER INFORMATION: Description of Artificial Sequence:Rana pipiens; OTHER INFORMATION: ribomuclease with Met at position 1 and Gln2Ser CTHER INFORMATION: substitution (recombinant Met (-1) RaPLR1 Q1S) US-09-948-391A-13
                            Sequence 13, Application US/09948391A

Sequence 13, Application US/09948391A

Sequence 13, Application US/09948391A

GENERAL INFORMATION:

APPLICANT: Rybak, Susanna M.

APPLICANT: The United States of America

APPLICANT: Department of Health and Human Services

TITLE OF INVENTION: Recombinant Anti-Tumor RNase

FILE REFERENCE: 015280-3431100S

CURRENT PILING DATE: 2002-05-10

PRIOR FILING DATE: 1998-03-27

PRIOR PILING DATE: 1998-03-27

PRIOR APPLICATION NUMBER: WO PCT/US99/06641

PRIOR APPLICATION NUMBER: WO PCT/US99/06641

PRIOR PILING DATE: 1999-03-26

PRIOR APPLICATION NUMBER: US 09/622,613

PRIOR FILING DATE: 2000-08-17

MUMBER OF SEQ ID NOS: 43

SEQ ID NO 13

TAPPE: Date IN DATE: 2001-08-17

LENGHI: 105

TAPPE: Date IN DATE: 2001-08-17

LENGHI: 105

TAPPE: Date IN DATE: 2001-08-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Artificial Sequence
RESULT 1
US-09-948-391A-13
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Gaps . 0 Query Match 100.0%; Score 582; DB 10; Length 105; Best Local Similarity 100.0%; Pred. No. 3.7e-59; Matches 105; Conservative 0; Mismatches 0; Indels 0;

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1 MSDWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLT

Search completed: May 7, 2004, 21:40:44 Job time: 12.1796 secs

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Gaps

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2 DWLIFPQKKHITNIRDVDCDNIMSTNLFHCKDKNTFIYSRPEPVKALCKGIIASKNVLTIS 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: PHARMACEUTICALS AND METHOD FOR MAKING THEM NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                    Length 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
94.7%; Score 551; DB 1;
Best Local Similarity 96.1%; Pred. No. 1.5e-59;
Matches 99; Conservative 2; Mismatches 2.
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PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 06-APR-1988
FRICA APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/814,332
FILING DATE: 03-FEB-1992
FRIJNG DATE: 01-ARG-1994
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US/08/467,955
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.24 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,95 FILING DATE:
         TELEPHONE: 718-625-0399
TELEFAX: 718-625-0399
TELEX: No. 5556734 Applicable
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE FRRACTERISTICS:
LENGTH: 104 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Ardelt Ph.D, Wojciech
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/08467955
Patent No. 5728805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSE: Mark H. Jay, P.A. STREET: P.O. BOX E CITY: Short Hills STATE: New Jersey
                                                                                                                                                                                                                                                                                                                              ORGANISM: Rana pipiens
DEVELOPMENTAL STAGE: Embryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Jay, Mark H.
REGISTRATION NUMBER: 27507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COINTRY: USA ZIP: 07078-0383
COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                  N-terminal
                                                                                                                                                                       single
                                                                                                                                                                                                              MOLECULE TYPE: protein HYPOTHETICAL: N
                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                        ANTI-SENSE: N
FRAGMENT TYPE: N
ORIGINAL SOURCE:
                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                            TOPOLOGY:
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US-08-467-955-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 DWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/07921619
Patent No. 5595734
GENERAL INFORMATION:
APPLICANT: Ardelt Ph.D, Wojciech J.
APPLICANT: Mikulski, Stanislaw M.
TITLE OF INVENTION: PHARMACEUTICAL FOR TREATING TUMORS IN HUMANS
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 104;
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CONTESTONDENCE ADDRESSES
STREET: P.O. Box 020083, General Post Office
CITY: Brooklyn
STATE: New York
COUNTRY: USA
ZIP: 11202-0002
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/921,619
FILING DATE: 19920728
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/178,118
FILING DATE: 06-APR-1988
PRICATION NUMBER: US 07/436,141
FILING DATE: 13-NOV-1989
ATTORNEY/AGENT INFORMATION:
ANAMERICATION NUMBER: US 07/436,141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 551; DB 1;
Pred. No. 1.5e-59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Mismatches
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REGISTRATION NUMBER: 27507
REFERENCE/DOCKET NUMBER: 5005 US
TELECOMMUNICATION INFORMATION:
FILING DATE: 13-NOV-1989
ATTORNEY/AGENT INFORMATION:
NAME: Jay, Mark H.
REGISTRATION NUMBER: 27507
REFERENCE/DOCKET NUMBER: 5006 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 718-625-0399
TELERA: No. 5529775 Applicable
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Rana pipiens
DEVELOPMENTAL STAGE: Embryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 94.7%;
Best Local Similarity 96.1%;
Matches 99; Conservative
                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 104 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                     ANTI-SENSE: N
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                  STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: N
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FILING DATE
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Pred. No. 1.9e-59;
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; Patent No. 6045793
; GENERAL INFORMATION:
    APPLICANT: Rybak, Susanna M.
    APPLICANT: Rybak, Lluis
    APPLICANT: Nodawer, Alexander
    TITLE OF INVENTION: Recombinant Ribonuclease Proteins
    VUMBER OF SEQUENCES: 64
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: Townsend and Townsend and Crew LLP
APPLICANT: Wlodawer, Alexander
IITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
                                                                                                                                                                                                                                          CONTON TYPE: P4111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPOTER: IBM PC compatible
OPERATIONS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
CLASSTRICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: REGISTRATION NUMBER: 41,739
REGISTRATION NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 015280-244100US
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Townsend and Townsend and Crew Lip
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
CTTF: California
COUNTRY: USA
                                                                                                 ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Enbarcadero Center, Bighth Floor STRY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 51:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      358 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 95.2
Matches 100; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; MOLECULE TYPE: protein US-08-875-811-51
                                                                         CORRESPONDENCE ADDRESS:
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  APPLICANT:
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1 MSDWLTFQKKHITNTRDVDCDNIMSTNLFHCKDKNTFTYSRPEPVKAICKGIIASKNVLT 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Ardelt Ph.D, Wojciech J.
APPLICANT: Mikuliski, Stanislaw M.
TITLE OF INVENTION: PHARMACEUTICAL FOR TREATING TUMORS IN HUMANS NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 TSEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TSEFYLSDCNVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Indels
COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/875,811 FILING DATE: 19-FEB-1998 CLASSIFICATION: 435 PRIOR APPLICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Mark H. Jay, P.C.
STREET: P.O. Box 020083, General Post Office
CITY: Brooklyn
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 555; DB 3;
Pred. No. 5e-60;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                            015280-244100US
                                                                                                                                                                                                             PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
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UMBER: US 07/178,118
06-APR-1988
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/921,180
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APPLICATION NUMBER: US 07/436,141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/283,971
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 5529775
                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 0152
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                               NAME: Faris, Susan K.
REGISTRATION NUMBER: 41,739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : 105 amino acids
amino acid
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Best Local Similarity 95.2
Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , MOLECULE TYPE: protein US-08-875-811-26
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ZIP: 11202-0002
COMPUTER READABLE FORM:
MEDIUM IYPE: Floppy
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61 TSEFYLSDCNVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 105
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0.
                                                                                                                       Sequence 41, Application US/08875811
Patent No. 6045793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 51, Application US/08875811; Patent No. 6045793; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Faris, Susan K.
REGISTRATION NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 01.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (415) 576-0300 INFORMATION FOR SEQ ID NO: 4 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : 355 amino acids
amino acid
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Best Local Similarity 95.23
Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                     San Francisco
California
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STATE:
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                                                                                                                                 3 DWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTTS
                                                                                                                                                                       2 DWLTPQKKHVTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTTS
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                                                                                                  Gaps
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                                                            Length 104;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 TSEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
                                                      Score 556; DB 1; Length 10
Pred. No. 3.7e-60;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                    63 EFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
                                                                                                                                                                                                                                                                                                                                           Sequence 39, Application US/08875811
Patent No. 6645793
GENERAL INFORMATION:
APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: Modawer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPOTER: IBM PC compatible
COMPOTER: IBM PC compatible
COMPOTER: IBM PC compatible
COMPOTER: IBM PC compatible
CURRENT APELICATION DATA:
APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
FILING DATE: 19-FEB-1997
FILING DATE: 19-FEB-1997
FILING DATE: 12-FEB-1997
APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 556; DB 3;
Pred. No. 3.8e-60;
2; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  015280-244100US
  Oocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: FATIS, SUSAN K.
REGISTRATION NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 01:
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (415) 576-0200
TELEPAX: (415) 576-0200
INPORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
                                                    Query Match
Best Local Similarity 97.1%;
Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : 105 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
DEVELOPMENTAL STAGE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  / MOLECULE TYPE: protein US-08-875-811-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: Two Embarcad
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 100; Conserv
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                                                                                                                                                                                                                                                                                                                          US-08-875-811-39
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  ;
US-08-467-955-2
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                                                      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Indels
GENERAL INFORMATION:
APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: Boque, Lluis
APPLICANT: Widdwer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/875,811
                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95.5%; Score 556; DB 3; 95.2%; Pred. No. 1.8e-59;
                                                                                                                                                                                                                                                                                                                                                                                                                                        ALFALICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: W0 PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAMM: Faris, Susar V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          015280-244100US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Mismatches
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Newton, Dianne L.
Boque, Lluis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
APPLICANT:
APPLICANT:
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COUNTRY: USA
ZIP: 07078-0383
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/178,118
FILING DATE: 06-APR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/436,141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Jay, Mark H.
REGISTRATION NUMBER: 27507
REFERENCE/DOCKET NUMBER: 5007 US
TELECOMUNICATION INFORMATION:
TELEPHONE: 201-912-9066
TELEFR: 201-912-9066
TELEFR: 205-912-9066
TELEFR: 805-912-9066
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-467-955-2; Sequence 2, Application US/08467955; Patent No. 5728805
                                                                                                 Query Match
Best Local Similarity 96.2%;
Matches 101; Conservative
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HYPOTHETICAL: N
ANTI-SENSE: N
                            ; MOLECULE TYPE: protein US-08-875-811-55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
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       linear
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ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
       TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MSDWLTFQKKHLTNTRDVDCNNIMSTNIFHCKDKNTFIYSRPEPVKAICKGIIASKNVLT 60
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                                                                                                                                                                                                                                                                                                                                                                                            96.2%; Score 560; DB 3; Length 355; 96.2%; Pred. No. 6e-60; tive 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 TSEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           311 TSEFYLSDCNVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Rybak, Susanna M.
APPLICANT: Rwbton, Dianne L.
APPLICANT: Boque, Lluis
APPLICANT: Wlodawer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER PAILLI-SOSA

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC Compatible
COMPUTER: ParentIn Release #1.0, Version #1.30
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
CLASSIFFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
FILING DATE: 19-FEB-1997
PRIOR APPLICATION DATA: REB-1996
ATTORNEY AGENT INFORMATION:
NAME: Faris, Susan K.
REGISTRATION NUMBER: 41,739
REGISTRATION NUMBER: 41,739
REGISTRATION NUMBER: 41,739
REGISTRATION NUMBER: 41,739
REGISTRATION NUMBER: 41,739
                                                                                                                                                                                                                                                                    NAME/KEY: Protein

LOCATION: 1..355

CHER INFORMATION: /note= "E6FB[Met-(-1)]Serronc"

US-08-875-811-6
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STREET: Two Enbarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            015280-244100US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 55, Application US/08875811; Patent No. 6045793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 0152
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
LENGTH: 366 amino acids
TELECOMMUNICATION INFORMATION:
TELERAX: (415) 576-0200
TELERAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : 366 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 96.2'
Matches 101, Conservative
                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 94111-3834
                                                                                                                                                                      STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-875-811-55
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                                                                                                                        1 MSDWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLT
                                                             0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL NO. 72809.

GENERAL INFORMATION:
APPLICANT: Ardelt Ph.D, Wojciech J.
TILLE OF INVENTION: PHARMACEUTICALS AND METHOD FOR MAKING THEM NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mark H. Jay, P.A.
STREET: P.O. BOX E
CITY: Short Hills
Score 560; DB 3; Length 366;
Pred. No. 6.2e-60;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                            322 TSEFYLSDCNVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 366
                                                                                                                                                                                                                                          61 TSEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 13-NOV-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/814,332
FILING DATE: 03-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/283,970
FILING DATE: 01-AUG-1994
ATTORNEY/AGENT INFORMATION:
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1 MSDWLTFQKKHITNTRDVDCDNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVII 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MSDWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96.2%; Score 560; DB 3; Length 355; 96.2%; Pred. No. 6e-60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 TSEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 64, Application US/08875811
Patent No. 6045793
GENERAL INFORMATION:
APPLICANT: Rybak, Susanna M.
APPLICANT: Nowton, Dianne L.
APPLICANT: Boque, Lluis
APPLICANT: Boque, Lluis
APPLICANT: Wlodawer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Townsend and Townsend and Crew LL STREET: Two Embarcadero Center, Eighth Floor STREET: San Prancisco STATE: California
              FILING DATE: 13.5

PRIOR APPLICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02589
FILING DATE: 19-FEB-1997

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Faris, Susan K.
REGISTRATION NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 015280-244100US
TELEPOMMUNICATION INPORMATION:
TELEPOMMUNICATION INPORMATION:
TELEPHONE: (415) 576-0300
TELEPRA: (415) 576-0300
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 015280-244100US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                          : 355 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best_Local Similarity 96.2
Matches 101; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-875-811-64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MSDWLIFQKKHLINTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 96.2%; Score 560; DB 3; Length 355; Best Local Similarity 96.2%; Pred. No. 6e-60; Matches 101; Conservative 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     311 TSBFYLSDCNVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 57, Application US/08875811
Fatent No. 6045793
GENERAL INFORMATION:
APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: Boque, Lluis
APPLICANT: Boque, Lluis
APPLICANT: Boque, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Bighth Floor
CITY: San Francisco
STATE: California
                                                                              COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: FROMS:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPATING SYSTEM: PC-DOS/WS-DOS
SOFTWARE: PATENTIN PC-DOS/WS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
PRIOR APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
CLASSIFICATION NUMBER: WO PCT/US97/02588
FILING BAPLICATION NUMBER: WO PCT/US97/02588
FILING BAPLICATION NUMBER: US 60/011,800
FILING BAPLICATION NUMBER: US 60/011,800
FILING BAPLICATION NUMBER: US 60/011,800
FILING BATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: FARISK SUBSAN K.
REGISTRATION NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 015280-244100US
TELEFPAN: (415) 576-0200
THELEFMAN: POS SEO 17 NO. 10
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CCMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CCMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
APPLICATION NUMBER: US/08/875,811
Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 49: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : 355 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; MOLECULE TYPE: protein US-08-875-811-49
                 San Francisco
California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
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                                                                  COUNTRY:
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Sat May

US-08-875-811-61

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                                                                                 8 MSDWLTFQKKHITNTRDVDCDNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLT 67
                                                1 MSDWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLT 60
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Pred. No. 3.8e-60;
2; Mismatches 2; Indels
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                                                                                                                                                                                          68 TSEFYLSDCNVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 112
                                                                                                                                              61 TSEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
  2; Indels
                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: Boque, Liuis
APPLICANT: Wlodawer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
UNDBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
CLASSIFICATION 3435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTONEY/AGENT INFORMATION:
ANNUMBER APPLICATION:
ANNUMBER APPLICATION:
ANNUMBER APPLICATION:
ANNUMBER APPLICATION:
ANNUMBER APPLICATION:
ANNUMBER APPLICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSE: Townsend and Townsend and Crew LLP STREET: Two Enbarcadero Center, Eighth Floor CITY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        015280-244100US
2; Mismatches
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                                                                                                                                                                                                                                                                                                               Sequence 59, Application US/08875811
Patent No. 6045793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY AVERAGE SUSAN K.
NAME: FAITS, SUSAN K.
REGISTRATION NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 0152
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (415) 576-0300 INFORMATION FOR SEQ ID NO: 59: SEQUENCE CHARACTERISTICS:
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amino acid
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Best Local Similarity 96.2<sup>3</sup>
Matches 101; Conservative
Matches 101; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
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GENERAL INFORMATION:
APPLICANT: Rybak,
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TOPOLOGY:
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US-08-875-811-59
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RESULT 3

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1 MSDWLTFQKKHITNTRDVDCDNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLT 60
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Patent No. 6045793
GENERAL INFORMATION:
APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: Modue, Lluis
APPLICANT: Moduer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
                                                                     APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: Boque, Lluis
APPLICANT: Wlodawer, Allaxander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PALENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Townsend and Townsend and Crew LLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 19-FEB-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION BATA:
APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
Sequence 61, Application US/08875811 Patent No. 6045793 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Faris, Susan K.
REGISTRATION NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 01:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (415) 576-0300 INPORMATION FOR SEQ ID NO: 6 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     254 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid
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                                                                                                                                                                                                                                                                                                                                                   USA
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7, 2004, 21:28:45 ; Search time 12.1796 Seconds (without alignments) 445.066 Million cell updates/sec
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1 MSDWLTFQKKHLTNTRDVDC.....TFCVTCENQAPVHFVGVGHC 105
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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    protein search,

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                                                                                                                                                            Title:
Perfect score:
                                                               OM protein
                                                                                                                                                                                             Sequence:
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389414 segs, 51625971 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

Scoring table:

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 200000000

1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:* Issued Patents AA:* Database

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Appl Appl Appl Appl Appl Appli Sequence 32, Sequence 59, Sequence 61, Sequence 57, Sequence 64, Sequence 64, Sequence 2, Assequence 2, Assequence 39, Description Sequence Sequence Sequence Sequence Sequence S Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence US-08-875-811-32
US-08-875-811-59
US-08-875-811-69
US-08-875-811-64
US-08-875-811-64
US-08-875-811-64
US-08-875-811-57
US-08-875-811-51
US-08-875-811-39
US-08-875-811-26
US-08-875-811-26
US-08-875-811-126
US-08-875-811-126
US-08-875-811-126
US-08-875-811-126
US-08-875-811-126
US-08-875-811-1 SUMMARIES Query Match Length Score No. Result

Length 112;

Score 560; DB 3; Pred. No. 1.3e-60;

96.2%; 96.2%;

Query Match Best Local Similarity

Sequence

53, 43,	Sequence 24, Appl Sequence 2, Appli	Sequence 2, Appli Sequence 2, Appli	7	Sequence 20, Appl	Sequence 47, Appl	Sequence 22, Appl	7	Sequence 3, Appli	3,	Sequence 12, Appl	Sequence 8, Appli	Sequence 4, Appli	Sequence 2, Appli	Sequence 1, Appli
US-08-875-811-53 US-08-875-811-43	US-08-875-811-24 US-08-626-288-2	US-09-095-429-2 US-09-394-268-2	US-09-687-748-2	US-08-875-811-20	US-08-875-811-47	US-08-875-811-22	US-08-875-811-2	US-09-071-672-3	US-09-986-119-3	US-08-891-848-12	US-08-875-811-8	US-09-223-118-4	US-09-223-118-2	US-09-223-118-1
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365	105	104	104	107	360	111	83	83	83	111	111	114	114	114
94.7	94.3 94.2	94.2 93.3	93.3	91.4	85.7	83.2	76.5	76.5	76.5	49.3	49.3	37.2	35.1	35.0
551 551	549 548	548 543	543	532	499	484.5	445	445	445	287	287	216.5	204.5	203.5
28	30 31	33 33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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R HSSP; P00656; J1520.

R InterPro; IPR001427; RNaseA.

R Pfam; PR00074; rnaseA.

R PRINTS; PR0074; RIBONUCLEASE.

R PRODOUS; PR00055; RNaseA; 1.

R SWART; SW00092; RNASE PC; 1.

R PROSITE; P800127; RNASE PC; 1.

T DISULFID 25 B0 BY SIMILARITY.

T DISULFID 39 91 BY SIMILARITY.

T DISULFID 57 106 BY SIMILARITY.

T ACT SITE 10 10 BY SIMILARITY.
                                                                                                                                                                                        Lur. J. Biochem. 219:641-646(1994).

-!- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
phosphates and 3'-phosphate intermediates.

-!- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
phosphates and 3'-phosphate intermediates.

-!- SUBCELLUIAR LOCATION: Secreted.

-!- TISSUE SPECIFICITY: Pancreas.

-!- SIMILARITY: Belongs to the pancreatic ribonuclease family.

PIR: $41111: $41111.

HSSP: P00656: 1LSQ.
Ribonuclease pancreatic (EC 3.1.27.5) (RNase 1) (RNase A).
Iguana iguana (Common iguana).
Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Iguania; Iguaniae; Iguaniae; Iguana.
                                                                                   [1] SQUENCE.
SEQUENCE.
MEDLINE=94139745; PubMed=8307028;
Zhao W., Baintema J.J., Hofsteenge J.;
"The amino acid sequence of iguana (Iguana iguana) pancreatic ribonuclease.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20.9%; Score 126.5; DB 1; Length 119; 29.8%; Pred. No. 8.4e-07; tive 16; Mismatches 51; Indels 13;
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les 34; Conservative
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91
106
10
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119 AA;
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Best Local S:
Matches 34
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61 GTHYEDNLYDSNESFDLTDCKNVGGTAPSSCKYNGTPGTKRIRIACENNQPVHF 114 Search completed: May 11, 2004, 14:35:05 Job time : 11.0452 secs g

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51; Indels 13; Gaps

53 -TGVINMNVLSTTRFQLNTCTRTSIT-PRPCPYSSRTETNYICVKCENQYPVHF 104

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151 AA.

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                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                            SEQUENCE OF 31-114 FROM N.A.
MEDLINE=93367815; PubMed=8356916;
MEDLINE=93367815; PubMed=8356916;
Breukelman H.J., Beintema J.J., Confalone E., Costanzo C., Sasso M.P., Carsana A., Palmiteri M., Friria A.;
"Sequences related to the ox pancreatic ribonuclease coding region in the genomic DNA of mammalian species.";
J. Mol. Evol. 37:29-35(1991).
-!- SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 ATFQQKHI-----INTPLICNTIMDNNIYIVGGQCKRVNTFLISSATTVKALCTGVINM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Giraffa camelopardalis (Giraffe).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Giraffoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Endonuclease; Glycoprotein.

1 BY SIMILARITY.

14 BY SIMILARITY.

15 BY SIMILARITY.

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12 BY SIMILARITY.

24 BY SIMILARITY.

25 N-LINKED (GLCNAC. . .) (BY SIMILARITY).
                                                                                                          SEQUENCE FROM N.A.
MEDLINE=96139017, PubMed=8587129;
Confalone E., Beintema J.J., Sasso M.P., Carsana A., Palmieri M.,
Vento M.T., Furia A.;
"Molecular evolution of genes encoding ribonucleases in ruminant
                                                                                                                                                                                                                                                                                                                  -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 141;
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30.6%; Pred. No. 7.8e-07;
 update)
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 Last annotation u
C 3.1.27.-) (BRB)
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PROSITE; PS00127; RNASE_PANCREATIC; 1.
16-OCT-2001 (Rel. 40, Last annotat
Ribonuclease, brain (EC 3.1.27.-)
                                                                                                                                                                                      Mol. Evol. 41:850-858(1995).
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PRINTS; PR00794; RIBONUCLEASE.
ProDom; PD000535; RNaseA; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001427; RNaseA.
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                                                              Mammalia; Eutheria;
Giraffidae; Giraffa.
                                                                                    NCBI_TaxID=9894;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                      Axis porcinus (Hog deer).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Cetartiodactyla, Ruminantia, Pecora, Cervoidea,
Cervidae, Cervinae, Axis.
                                                                                                                                                                                                                                                                                                                                                                                                         Secretory ribonuclease genes and pseudogenes in true ruminants."; gene 212:259-268(1998).
                                                                                                                                                                                                                                                                                                                    MEDLINE-98278842; PubMed-9611269;
Breukelman H.J., van der Munnik N., Kleineidam R.G., Furia A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
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84 BY SIMILARITY.

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62 N-LINKED (GLCNAC. . .) (BY SIMILARITY.

129 O-LINKED (BY SIMILARITY).

131 O-LINKED (BY SIMILARITY).

131 O-LINKED (BY SIMILARITY).

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N-LINKED (GLCNAC. . .) (B)
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Pred. No. 8.4e-07;
                   15-DEC-1998 (Rel. 37, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Ribonuclease, brain (EC 3.1.27.-) (BRB).
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PRINTS; PR00794; RIBONUCLEASE.
ProDom; PD000535; RNaseA; 1.
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last seg
28-FEB-2003 (Rel. 41, Last ann
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30.6%;
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PROSITE; PS00127; RNASE PAN
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                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                           NCBI_TaxID=57737;
                                                                                                                                                                                                                                                                                                                                                                                  Beintema J.J.;
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P80<u>2</u>87;
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RNBR_AXIPR RESULT 14

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59 NVL-----STTRFQLNTCTRTSITPRP-CPYSSRTETNYICVKCENQ--YPVHF 104
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tive 19; Mismatches
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                                                                                                                                                POROHADDSSSSNSSNYCNIAMSRR-NWTQGRCKPVNTFVHESLADVQAVCSQINVNCK 66
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                                                                                                                  7 FOOKHI-----INTPIICUTIMDNNIYIVGGOCKRVNTFIISSATTVKAICTGV-INMN 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 ATFQQKHI-----INTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINM 58
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                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                    15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
Capreolus capreolus (Roe deer).
Capreolus capreolus (Roe deer).
Bukaaryota, Metazoa, Chordata, Craniata, Vertebrata; Buteleostomi;
Cervidae; Odocoileinae; Capreolus.
                                                                                                                                                                                               104
                                                                                                                                                                                                                                    67 NGQTNCYQSNSTMHITDCRQTGSSKYPNCAYKASQEQKHIIVACEGNPPVPVHF 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Secretory ribonuclease genes and pseudogenes in true ruminants.";
                                                                                                                                                                                               60 VLSTTRFQLNT-----CTRTSITPRP-CPYSSRTETNYICVKCENQ--YPVHF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23;
                                                                           17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Breukelman H.J., van der Munnik N., Kleineidam R.G., Furia A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gene 212:259-268(1998).
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
                                        Length 124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 151;
                                                                             Indels
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W; 392DDE6302F006A6 CRC64;
0AC28CDE14111845 CRC64;
                      21.9%; Score 132.5; DB 1;
31.6%; Pred. No. 2e-07;
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29.4%; Pred. No. 6.6e-07;
                                                                                                                                                                                                                                                                                                                                      151 AA
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PROSITE; PS00127; RNASE_PANCREATIC; 1.
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Pfam; PF00074; rnaseA, 1.
PRINTS; PR00794; RIBONUCLEASE.
ProDom; PD000535; RNaseA, 1.
13804 MW;
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                                                                                                                                                                                                                                                                                                                                      STANDARD;
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84
95
110
  124 AA;
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                                                     Local Similarity
es 36; Conserv
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nes 35; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9858;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-974(9980, PubMed-9266695, Strydom D.J., Bond M.D., Vallee B.L.;

An angiogenic protein from hovine serum and milk -- purification as primary structure of angiogenin-2.",

Eur. J. Biochem. 247:535-544(1997).

-!- FUNCTION: Binds tightly to placental ribonuclease inhibitor and has very low ribonuclease activity. Has potent angiogenic activity. Angiogenin induces vascularization of normal and malignant tissues. Abolishes protein synthesis by specifically hydrolyzing cellular tRNAs.

-!- TISSUE SPECIFICITY: Serum and milk.

-!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Merazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66 NGLRRSRSPFQVTTCRHRGGSPRPPCRYRAFRANRVIVIRCRDGFPIH 113
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B703B9839919FD2F CRC64;
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HSSP, PULLS.
HSSP, PULLS.
InterPro, IPR01427; RNaseA.
FRIMTS, PR0074; INSEAN.
PRODOM; PR00794; RIBONUCLEASE.
ProDom; PR00795; RNaseA; 1.
SWART; SW00092; RNAse Pc; 1.
SWART; SR00102; RNAse Pc; 1.
PROSITE: PS00127; RNAse Pc; 1.
Procin synthesis inhibitor; Glycoprotein;
Pyrroliace; Nuclease; Endonuclease; Angiogenesis;
Pyrtein synthesis inhibitor; Glycoprotein;
MOD_RES
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Pred. No. 6.8e-07;
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MEDLINE=70104197; PubMed=5460946;
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InterPro; IPR001427; RNaseA.
    Conservative
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                                                                                                                                         59 NVL----
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  38;
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                                                                                                                                                                                                                                                            Sasso M.P., Carsana A., Confalone B., Cosi C., Sorrentino S.,
Viola M., Palmieri M., Russo B., Furia A.;
"Moclecular cloning of the gene encoding the bovine brain ribonuclease
and its expression in different regions of the brain.";
Nucleic Acids Res. 19:6469-6474(1991).
                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae, Bovinae, Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Watanabe H., Katoh H., Ishii M., Komoda Y., Sanda A., Takizawa Y., Obgi K., Irie M.; "Primary structure of a ribonuclease from bovine brain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=96139017; PubMed=8587129; Octalone E., Beintema J.J., Sasso M.P., Carsana A., Palmieri M., Vento M.T., Furia A.; Molecular evolution of genes encoding ribonucleases in ruminant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            J. Mol. Evol. 41:850-858(1995).
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
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681CAAC3CC2FC459 CRC64;
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N-LINKED (GLONAC. . . ).
/FIId=CAR_000005.
                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 27-167, AND CARBOHYDRATE-LINKAGE SITES
16-OCT-2001 (Rel. 40, Last annotation update)
Ribonuclease, brain precursor (RC 3.1.27.-) (BRB)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch)
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SMART; SM00092; RNASe Pc; 1.
PROSITE; PS00127; RNASE PANCREATIC; 1.
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                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=92093604; PubMed=1754384;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=89214015; PubMed=3243767;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J. Biochem. 104:939-945(1988).
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PRINTS; PR00794; RIBONUCLEASE.
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31.4%;
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HSSP; P00656; ZRNS.
GlycoSuiteDB; P39873; -.
InterPro; IPR001427; RNaseA.
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159
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167 AA;
                                                                          taurus (Bovine)
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Best Local Similarity
                                                                                                                                                                  NCBI_TaxID=9913;
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                                                                                         --STIRFQLNICIRISIIPRP-CPYSSRIEINYICVKCE-NQY-PVHFA 105
                                                                                                                      88 NITCKNGHPNCYQSKSTMSITDCRETGSSKYPNCAYKTSQKQKYITVACEGNPYVPVHFD 147
                              5 ATFQQKHI-----INTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINM 58
                                                           32 AKFRROHMDSGSSSSSNPNYCNOMMKRR-RMTHGRCKPVNTFVHESLDDVKAVCS---QK 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wierenga R.K., Huizinga J.D., Gaastra W., Welling G.W., Beintema J.J., "Affinity chromatography of porcine pancreatic ribonuclease and reinvestigation of the N-terminal amino acid sequence."; FEBS Lett. 31:181-185(1973).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J. Biol. Chem. 245:654-661 (1970).
-!- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
phosphates and 3'-phosphooligonucleotides ending in C-P or U-P
with 2',3'-cyclic phosphate intermediates.
-!- SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                      Sus scrofa (Pig).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Jackson R.L., Hirs C.H.W.;
"The primary structure of porcine pancreatic ribonuclease. II.
amino acid sequence of the reduced S-aminoethylated protein.";
J. Biol. Chem. 245:637-653(1970).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=70104198; PubMed=4904878;
Phelan J.J., Hirs C.H.W.;
"The primary structure of porcine pancreatic ribonuclease. 3.
disulfide bonds.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -i-TISSUE SPECIFICITY: Pancreas.
                                                                                                                                                                                                                                                                                           21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
28-FRB-2003 (Rel. 41, Last annotation update)
Ribonuclease pancreatic (EC 3.1.27.5) (RNase 1) (RNase A)
 43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BY SIMILARITY.
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N-LINKED (GLCNAC..
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                                                                                                                                                                                                                                                                124 AA.
 17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS, PRO0794, RIBONUCLEASE.
ProDom, PD000535, RNASEA. 1.
SWART, SM00092, RNASE PC, 1.
PROSITE, PS00127, RNASE PANCREATIC, 1.
HYdrolase, Nuclease, Endonuclease; Gly
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CARBOHYD
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human and mouse cDNA sequences.";
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ARAINTENDY, N. 11220-11477932,

ALTAINTENDY, N. 11220-11477932,

ALTAINTENDY, OTGING E.A., Grouse L.H., Derge J.G.,

ALTAINTENDY B. D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetcow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

ALTSCHUL S. F., Zeeberg B. B., Bonaldow M.F., Casavant T.L., Scheetz T.E.,

B. Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

B. Stapleton M., Soares M.B., Donaldow M.F., Casavant T.L., Scheetz T.E.,

B. Rohastein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

B. Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

B. Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

W. Ilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

B. Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                     09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      64 LCKNGRTNCYESNSTMHITDCRQTGSSKYPNCAYKTSQKEKHIIVACEGNPYVPVHF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                  61 L-----STTRFQLNTCTRTSITPRP-CPYSSRTETNYICVKCE-NQY-PVHF 104
                                                                                                                                                                                                                                                                                                                                                                   7 FQQKHII------NTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNV
                                                                                                                                                                                                                                                                                                                                                                                                 8 FOROHMDSGNSPGNNPNYCNOMMARR-KMTOGRCKPVNTFVHESLEDVKAVCS---OKNV
                                                                                                                                                                                                                                                                                                                                      23; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-WAY-1991 (Rel. 18, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
Angiogenin precursor (EC 3.1.27.-) (Ribonuclease 5) (RNase 5).
                                                                                                                                                                                                                                                                                                        DB 1; Length 124;
                                                                                                                                                                                                                                                        .) (30%).
                                                                                                                                       95 BY SIMILARITY.
96 BY SIMILARITY.
110 BY SIMILARITY.
72 BY SIMILARITY.
12 BY SIMILARITY.
14 BY SIMILARITY.
119 BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                   ; Pred. No. 9.4e-08;
16; Mismatches 39;
                                                                                                                             Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                145 AA
                                                                                                                                                                                                                                                                                                          22.4%; Score 135.5;
             HSSP; P00656; ISRN.
InterPro; IPR001427; RNaseA.
Fida, PF00074; rnaseA; 1.
FRINTS; PR00794; RIBONUCLEASE.
ProDom; PD000535; RNaseA; 1.
SMART; SM00092; RNASE PC; 1.
FROSITE; PS00127; RNASE PC; 1.
Hydrolase; Nuclease; Endonuclease; Glyco
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                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 33.33
Matches 39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
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41
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PIR; A00818; NRWHK
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P21570;
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                                                                                                                                             Gaps
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PRODOM; PRO01515; RNaseA; 1.
PRODOM; PO000515; RNAse Pc; 1.
PROSITE; PS00127; RNASE Pc; 1.
Hydrolase; Nuclease; Endonuclease; Anglogenesis;
Protein synthesis inhibitor; Signal; Pyrrolidone carboxylic acid.
                                                                        MEDLINE=93192291; PubMed=8448182;
Bond M.D., Strydom D.J., Vallee B.L.;
"Characterization and sequencing of rabbit, pig and mouse
angiogenins: discernment of functionally important residues and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       39.5%; Pred. No. 1.1e-07; ive 12; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06944260BB764938 CRC64;
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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(Rel. 31, Last sequence update)
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123 FRHVVIACENGLPVHF 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MGD; MGI:88022; Ang.
InterPro; IPR001427; RNaseA.
Pfam; PF00074; rnaseA; 1.
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                                    PARTIAL SEQUENCE.
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81
                                                         TISSUE=Serum;
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01-FEB-1995
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ID RNBR_BOVIN
AC P39873;
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33; Conservative
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25
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64
137
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P00673;
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DISULFID
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MOD RES
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                                                                                                                entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                               ıt is in no way
and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                         63 CKEVNTFIHDTKNNIKAICGENGRPYGV-NFRI-SNSRFQVTTCTHKGGSPRPPCQYNAF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                              34 CKRVNTFIISSATTVKAIC-----TGVINMNVLSTTRFQLNTCTRTSITPR-PCPYSSR 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=129; TISSUB=Liver; MEDLINE=96079109; PubMed=8530072; Brown W.E., Noblie V., Subramanian V., Shapiro R.; Brown W.E., noblie V., Subramanian V., Shapiro R.; The mouse anglogenin gene family: structures of an angiogenin-related protein gene and two pseudogenes."; Genomics 29:200-206(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                          9; Gaps
                           -:- FUNCTION: Angiogenin induces vascularization of normal and malignant tissues. Abolishes protein synthesis by specifically hydrolyzing cellular tRNAs (By similarity)
-:- SIMILARITY: Belongs to the pancreatic ribonuclease family.
                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                      25.5%; Score 154.5; DB 1; Length 145;
 developmentally regulated genes when expressed in NIH 3T3
                                                                                                                                                                                                                                                                                     ANGIOGENIN-3.
PYRROLIDONE CARBOXYLIC ACID
(BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                         23; Indels
                                                                                                                                                                                                                                                                                                                                                                                   DE9D3BC92F1D682C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                               1e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1997 (Rel. 35, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Anglogenin-related protein precursor.
                                                                                                             use by non-profit institutions as long a modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            145 AA.
                                                                                                                                                                                                                                                                                                                    BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                        12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No.
                   Biol. 17:1503-1512(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    87 TETNYICVKCENOYPVHF 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 KDFRYİVIACEDGWEVHF 138
                                                                                                                                                                                  MGD; MGI:1201793; Angl.
InterPro: IFRO01427; RNBSEA.
Pfam; PF00074; rnaseA; 1.
PRINTS; PR00794; RIBONUCLEASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1997 (Rel. 35, Created)
                                                                                                                                                                                                                                                                                                                                                                                  16696 MW;
                                                                                                                                                              EMBL; U72672; AAC05794.1; -. HSSP; P10152; 1AGI.
                                                                                                                                                                                                                                                                                                                                                                                                               43.68;
                                                                                                                                                                                                                           PD000535; RNaseA; 1
                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                         137
104
115
130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                    37
64
137
50
13
63
145 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
          fibroblasts."
                                                                                                                                                                                                                                                                                                                                                                                                                        34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ANGR MOUSE
Q64438;
                                                                                                                                                                                                                                                                                                                                                  DISÜLFID
DISULFID
                                                                                                                                                                                                                                                                                                                       SILE
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                                                                                                                                                                                                                                                                                                                                                                        DISULFID
                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                          ProDom;
                                                                                                                                                                                                                                                                                                  MOD RES
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOUSE
                                                                                                                                                                                                                                                                                                                    ACT
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropan Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseaisb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63 CKDVNTFIHDTKANIKAICGKKGSPYGRNLRISKSRFQVTTCTHKGRSPRPCRYRASKG 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34 CKRVNTFIISSATTVKAIC---TGVINMNV-LSTTRFQLNTCTRISITPR-PCPYSSRTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ribonuclease.";
Biochem G. 157:317-323(1976).
-!- CAPALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
phosphates and 3'-phosphooligonucleotides ending in C-P or U-P
with 2', 3'-cyllic phosphate intermediates.
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Pancreas.
-!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Emmens M., Welling G.W., Beintema J.J.;
"The amino acid sequence of pike-whale (lesser-rorqual) pancreatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Balaenoptera acutorostrata (Minke whale) (Lesser rorqual).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Cetartiodactyla; Cetacea; Mysticeti;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2;
SIMILARITY: Belongs to the pancreatic ribonuclease family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24.7%; Score 149.5; DB 1; Length 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PYRROLIDONE CARBOXYLIC ACID (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
Ribonuclease pancreatic (EC 3.1.27.5) (RNase 1) (RNase A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ANGIOGENIN-RELATED PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29A6EB814429C4AD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 3.5e-09;
                                                                                                                                                                                                                                                                                                                                                                                           MGD; MGI:104984; Angrp.
InterPro; IPR001427; RNSSAA.
PRAM; PR00074; TNBSEA, 1.
PRINTS; PR00794; RIBONUCLEASE.
ProDom; PD000535; RNSSAA; 1.
SMART; SM00092; RNASSE, 1.
PROSITE; PS00127; RNASE Po; 1.
PROSITE; PS00127; RNASE PanCREATIC; 1.
Signal, Hydrolase; Nuclease;
Pyrrolidone carboxylic acid.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     124 AA.
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BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16612 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Balaenopteridae; Balaenoptera.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              123 FRYIIIGCENGWPVHF 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                89 TNYICVKCENQYPVHF 104
                                                                                                                                                                                                                                                                                                                               EMBL; U22519; AAA91367.1; -. HSSP; P03950; 1A4Y.
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3 NWATFQQKHIINT-PIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NMNV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DWLTFQKKHITNTRDVDCDNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKNV 57
-!- FUNCTION: Basic protein with antiproliferative/cytotoxic activity
                                             molecular weight ribosomal RNA.
-!- DEVELOPMENTAL STAGE: Early embryos (up to four blastomere stage).
-!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
                ainst several tumor cell lines in vitro, as well as antitumor vivo. It exhibits a ribonuclease-like activity against high
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Rel. 35, Created)
(Rel. 35, Last sequence update)
(Rel. 41, Last sequence update)
(Rel. 41, Last sequence of protein 2)
precursor (EC 3.1.27.-) (Angiogenin-related protein 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fu X., Kamps M.P.; "E2a-Pbx1 induces aberrant expression of tissue-specific and
                                                                                                                                                                                                                      PYRROLIDONE CARBOXYLIC ACID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22A753C2F9E566B4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    45.0%; Score 272.5; DB 1;
49.1%; Pred. No. 1.4e-22;
iive 15; Mismatches 32;
                                                                                                                                                                                       Hydrolase; Nuclease; Endonuclease; 3D-structure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           145 AA
                                                                                                                                         ProDom, PD000535; RNaseA; 1.
SMART; SM00092; RNASE PC; 1.
PROSITE; PS00127; RNASE_PANCREATIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=97184476; PubMed=9032278;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11845 MW;
                                                                                           PDB; IONC; 31-JAN-94.
InterPro; IPR001427; RNaseA.
                                                                                                                                                                                                            acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   54; Conservative
                                                                                                                          Pfam; PF00074; rnaseA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                         Pyrrolidone carboxylic
                                                                                                                                                                                                                                                                       Mus musculus (Mouse)
                  against several
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        104 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10090;
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31
31
119
119
87
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P97802;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NCV-1997
28-FEB-2003
                                                                                                                                                                                                                                                                                                                  DISULFID
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DISÜLFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                             3 NWATFQQKHIINTPII-CNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NMNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 NWAKFKEKHIRSTSSIDCNTIMDKAIYIVGGKCKERNTFIISSEDNVKAICSGVSPDRKE
                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Comparative molecular modeling and crystallization of P-30 protein:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDILINE=94166079; PubMed=8120892;
Mosimann S.C., Ardelt W., James M.N.G.;
"Refined 1.7 A X-ray crystallographic structure of P-30 protein, an amphibian ribonuclease with anti-tumor activity.";
J. Mol. Biol. 236:1141-1153(1994).

    CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-phosphates and 3'-phosphate intermediates ending in C-P or U-P with 2', 3'-cyclic phosphate intermediates.
    SUBCELLULAR LOCATION: Secreted.
    SIMILARITY: Belongs to the pancreatic ribonuclease family.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Embryo;
MEDLINE=91093131; PubMed=1985896;
Ardelt W., Mikulski S.M., Shogen K.;
Andelt w., Mikulski S.M., Shogen K.;
"Amino acid sequence of an anti-tumor protein from Rana pipiens cocytes and early embryos. Homology to pancreatic ribonucleases.";
J. Biol. Chem. 266:245-251(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-AUG-1991 (Rel. 19, Created)
01-FBB-1994 (Rel. 28, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
P-30 protein (EC 3.1.27.-) (Onconase).
P-30 protein (EC 3.1.27.-) (Onconase).
Entary pictor (EC 3.1.27.-) (Onconase).
Entary pictor (EC 3.1.27.-) (Onconase).
Entary ota , Metazoa; (Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 LSTTRFQLNTCTRTSITPRPCPYSSRTEINYICVKCENQYPVHFAGIGRC 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62 LSTISFKLNTCIRDSITPRPCPYHPSPDNNKICVKCEKQLPVHFVGIGKC 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=93066156; PubMed=143817;
Mosimann S.C., Johns K.L., Ardelt W., Mikulski S.M., Shogen K.,
                                                                                                                                                                                                       2;
                                                                                                                                                                                                                                                                                                                                                                                Length 111;
                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                    D64BA72456C10788 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                               27;
                                                                                                                                                                                                                                                                                                                                                                                Score 369; DB 1;
Pred. No. 6.4e-33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         104 AA
                                                                                                                                                                                                                                                                                                                                                                                                                 9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS).
                                                                                                                                                                                          PANCREATIC; 1.
                                                                                                                                                                                                                                                                                                                                                   12461 MW;
   106:729-735 (1989)
                                                                                                                          InterPro; IPR001427; RNaseA.
Pfam; PF00074; rnaseA; 1.
                                                                                                                                                          ProDom; PD000535; RNaseA; 1.
SMART; SM00092; RNASE PC; 1.
PROSITE; PS00127; RNASE PANCI
                                                                                                                                                                                                                                                                                                                                                                                60.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Proteins 14:392-400(1992).
                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 65...
72; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3D-STRUCTURE MODELING.
                                                                                               PIR; JX0085; JX0085.
HSSP; P11916; 1BC4.
                                                                                                                                                                                                                                                                                                                                                    AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=8404;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     James M.N.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RANPI
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                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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T 4 RANPI RN30 RA P22069;

à П ð d 4;

Gaps

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RNPL_RANCA
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                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              83
residues with a 3'flanking guanine. Hydrolyzes poly(U) and poly(C) as substrates, and prefers the former. The S-lectins in frog eggs may be involved in the fertilization and development of the frog embryo. This lectin agglutinates various animal cells, including normal lymphocytes, erythrocytes, and fibroblasts of animal and human origin. It is cytotoxic against several tumor cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 NWAIFQOKHIINTPII-CNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART; SW00092; RNASE PC; 1.
PROSITE; PS00127; RNASE PANCREATIC; 1.
Hydrolase; Nuclease; Endonuclease; Sialic acid; Lectin; 3D-structure; Signal; Pyrrolidone carboxylic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STTRFQLNTCTRTSITPRPCPYSSRIETNYICVKCENQYPVHFAGIGRCP 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENOYPVHFAGIGRCP 133
                                                                    SUBCELLULAR LOCATION: Secreted. SIMILARITY: Belongs to the pancreatic ribonuclease family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96.8%; Score 586.5; DB 1; Length 133; 99.1%; Pred. No. 3.1e-56;
                                                                                                                                                                                                                                                                                                           RIBONUCLEASE, OOCYTES.
PYRROLIDONE CARBOXYLIC ACID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14762 MW; A7D62594F7D16F0C CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Rel. 16, Created)
(Rel. 28, Last seq.
(Rel. 42, Last anno
                                                                                                                                                                                   EMBL; AF039104; AAD10702.1; -.
                                                                                                                                                                                           PIR; A27121; A27121.
PDB; 1BC4; 28-OCT-98.
PDB; 1MO7; 21-JAN-09.
InterPro; IPR01427; RNaseA.
Pfam; PF00074; rnaseA; 1.
ProDom; P0000535; RNaseA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                  22
133
23
32
32
57
125
103
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63
74
74
84
95
                                                              SUBUNIT: Monomer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             133 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1990
01-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Sim
Matches 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LECS RANJA
P18839;
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ACT_SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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Last sequence update) Last annotation update)

10-OCT-2003

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61
                                                                                                                                                                                                                                                                 FUNCTION: The S-lections in frog eggs may be involved in the fertilization and development of the frog embryo. This lectin preferentially agglutinate a large variety of tumor cells, but it does not agglutinate non-transformed cells and erythrocytes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Primary structure of a ribonuclease from bullfrog (Rana catesbeiana)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                    TISSUE=Egg;
MEDLINE=91035319; PubMed=2229005;
Kamiya Y., Oyama F., Oyama R., Sakakibara F., Nitta K., Kawauchi H.,
Takayanagi Y., Titani K.;
                                                                                                                                                                                                                Amino acid sequence of a lectin from Japanese frog (Rana japonica)
Sialic acid-binding lectin (EC 3.1.27.-).
Rana japonica (Japanese reddish frog).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia: Batrachia; Anura; Neobatrachia; Ranoidea; Raniae; Rana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ania calebbrama buli 1993.
Eukaryota, Mecazoa; Chordata; Craniata; Vertebrata; Euteleogtomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 LSTTRFQLNTCTRISITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nitta R., Katayama N., Okabe Y., Iwama M., Watanabe H., Abe Y., Okazaki T., Ohgi K., Irie M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2;
                                                                                                                                                                                                                                                                                                                                                                         -!- SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          74.3%; Score 450; DB 1; Length 111; 78.2%; Pred. No. 1.2e-41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PYRROLIDONE CARBOXYLIC ACID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001427; RNaseA.
Pfam; PF00074; TnaseA; 1.
Srobom; PR000055; RNaseA; 1.
SMART; SM00092; RNASe Pc; 1.
SROSI127; RNASE PANCREATIC; 1.
Hydrolase; Nuclease; Endonuclease; Sialic acid; Lectin; Pyrrolidone carboxylic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12326 MW; FDEBDDF3834ED679 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-APR-1990 (Rel. 14, Created)
01-FBR-1994 (Rel. 28, Last sequence update)
28-FBR-2003 (Rel. 41, Last annotation update)
18-Ebronuclease, liver (EC 3.1.27.5).
Rana catesbeiana (Bull frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY.
SIMILARITY.
SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=90130374; PubMed=2613682;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BY
BY
BY
                                                                                                                    SEQUENCE, AND DISULFIDE BONDS.
                                                                                                                                                                                                                                                           J. Biochem. 108:139-143(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10
35
104
72
                                                                                                                                                                                                                                                                                                                                                                                                                PIR; JX0120; JX0120.
HSSP; P11916; 1BC4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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                                                                             NCBI_TaxID=8402;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35
104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rissum=Liver;
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

May 11, 2004, 14:24:28 ; Search time 10.0452 Seconds (without alignments) 575.375 Million cell updates/sec Run on:

US-09-961-400-26 606 1 MSNWATFQQKHIINTPIICN.....ICVKCENQYPVHFAGIGRCP 111 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 seqs, 52070155 residues Searched:

141681 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

SwissProt_42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	rana	P18839 rana japoni	rana	rana	mus m		bala		P39873 bos taurus										-	P00668 antilocapra	P00686 macropus ru	P00676 myocastor c		_			-		-	Ö	9 proe	_	Q8wn63 macaca mula
SUMMARIES	ΩI		LECS RANJA		RN30 RANPI	ANG3 MOUSE	ANGR MOUSE	RNP BALAC	ANGI MOUSE	RNBR_BOVIN	RNP PIG	RNBR CAPCA	ANG2_BOVIN	RNBR_GIRCA	RNBR AXIPR	RNP IGUIG	ANGI CERAE	ANGI_MIOTA		RNBR_SHEEP	RNP ANTAM	RNP_MACRU	RNP_MYOCO	ANGI PONPY	RNP_MOUSE	ANGI_AOTTR	ANGI_PIG		ANGI_SAGOE		RNP CAMDR			ANGI_MACMU
	DB	-	П	Н	Н	Н	Н	Н	Н	7	Н	Н	Н	н	Н	Н	П	-	Н	Н	Н	П	1	Н	Н	1	Н	Н	Н	н	Н	Н	Н	7
	Length	133	111	111	104	145	145	124	145	167	124	151	123	141	151	119	146	146	146	143	124	122	128	147	4	4	123	2	146	128	124	128	119	146
۰\٠	Query Match	8.96	74.3	6.09	45.0	25.5	24.7	22.4	22.4	22.0	21.9	21.2	21.0	21.0	21.0	20.9	20.9	20.9	20.6	20.4	20.3	20.1	19.9	19.9	19.9	19.8	19.7	19.6	19.5	19.4	19.2	19.2	19.1	19.1
	Score	586.5	450	369	272.5	154.5	149.5	135.5	135.5	133.5	132.5	128.5	127.5	127.5	127.5	126.5	126.5	126.5	125	123.5	122.5	122	120.5	120.5	120.5	120	119.5	118.5	118	117.5	116.5	116.5	115.5	115.5
	Result No.	1	7	e	4	2	9	7	8	σ	10	11	12	13	14	1.5	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33

P10152 bos taurus	P00666 rangifer ta	P31347 oryctolagus	Q8wn64 papio hamad	P03950 homo sapien	Q8wme8 pan troglod	P00664 capreolus c	P00662 giraffa cam	Q9jjhl mus musculu	P24717 cricetulus	OS5004 rattus norv	Q9wtt5 acomys cahi
ANGI BOVIN	RNP RANTA	ANGI RABIT	ANGI PAPHA	ANGI HUMAN	ANGI PANTR	RNP CAPCA	RNP_GIRCA	RNS4 MOUSE	RNP CRILO	RNS4 RAT	RNP_ACOCA
Н	Н	Н	Н	Н	Н	Н	Н	Н	Т	٦	Н
148	124	125	146	147	147	124	124	148	130	147	149
18.8	18.7	18.7	18.7	18.6	18.6	18.6	18.6	18.6	18.4	18.4	18.4
114	113.5	113.5	113.5	113	113	112.5	112.5	112.5	111.5	111.5	111.5
34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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1 SNWATFQQKHIINT-PIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NNN 58
                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Artificial Sequence
; PEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Rana pipiens
; OTHER INFORMATION: ribonuclease with GlaiSer substitution
; OTHER INFORMATION: (recombinant RapIR1 Q1S)
US-09-948-391A-11
                                                                                                                                                                                                         Query Match
Best Local Similarity 49.5%; Pred. No. 4.5e-24;
Matches 55; Conservative 15; Mismatches 32; Indels 9;
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4.

9; Gaps

Search completed: May 11, 2004, 14:39:23 Job time : 38.8281 secs

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69 TTRFQLNTCTRISITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 117

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2 NWATFQQKHIIKTPIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINLNVLS 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 NWATFQQKHIINTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNVLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTRPQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTRFQLNTCTRISITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Description of Artificial Sequence:Rana OTHER INFORMATION: catesbeiana ribonuclease with Met22Leu and OTHER INFORMATION: Met57Leu substitutions (recombinant RaCORI OTHER INFORMATION: Met22Leu Met57Leu)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
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APPLICANT: The United States of America
APPLICANT: The United States of America
APPLICANT: Serepresented by The Secretary of the
APPLICANT: Serepresented by The Secretary of the
APPLICANT: Department of Health and Human Services
TITLE OF INVENTION: Recombinant Anti-Tumor RNase
FILE REFERENCE: 015280-34110US
CURRENT APPLICATION NUMBER: US/09/948,391A
CURRENT FILING DATE: 2002-05-10
PRIOR APPLICATION NUMBER: WG PCT/US99/06641
PRIOR APPLICATION NUMBER: WG PCT/US99/06641
PRIOR APPLICATION NUMBER: WG PCT/US99/06641
PRIOR FILING DATE: 1999-03-26
PRIOR APPLICATION NUMBER: US 09/622,613
PRIOR APPLICATION NUMBER: US 09/622,613
PRIOR APPLICATION NUMBER: US 09/622,613
PRIOR APPLICATION NUMBER: US 09/622,613
PRIOR APPLICATION NUMBER: US 09/622,613
PRIOR APPLICATION NUMBER: US 09/622,613
PRIOR APPLICATION NUMBER: US 09/622,613
PRIOR APPLICATION NUMBER: US 09/622,613
                                                                                                                                                                                                                                                                                                                             APPLICANT: Newton, Dianne L.
APPLICANT: The United States of America
APPLICANT: The United States of America
APPLICANT: The United States of America
APPLICANT: The United States of America
TITLE OF INVENTION: Recombinant Anti-Tumor RNase
FILE REFERENCE: 015200-34311008 948,391A
CURRENT APPLICATION NUMBER: US/09/948,391A
CURRENT FILING DATE: 2002-05-10
PRIOR FILING DATE: 1998-03-27
PRIOR FILING DATE: 1998-03-27
PRIOR FILING DATE: 1998-03-26
PRIOR FILING DATE: 1998-03-26
PRIOR FILING DATE: 2000-08-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 10;
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97.2%; Pred. No. 1.2e-58;
iive 2; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 11, Application US/09948391A; Publication No. US20030027311A1; GENERAL INFORMATION:
                                                                                                                                                                                  ; Sequence 19, Application US/09948391A
                                                                                                                                                                                                                      Publication No. US20030027311A1
GENERAL INFORMATION:
APPLICANT: Rybak, Susanna M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 106; Conservative
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                                                                                                           RESULT 14
US-09-948-391A-19
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publication No. US20030124131A1

general information:

general information:

general information:

general information:

APPLICANT: RTAMA, SUSANNA M.

APPLICANT: NEWTON, DIANNE L.

TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT;

TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT;

TITLE OF INVENTION: UNMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT;

FILE REFERENCE: 018733/1059

CURRENT FILING DATE: 2001-09-25

PRIOR APPLICATION NUMBER: 05/622,613

PRIOR FILING DATE: 1999-03-26

PRIOR FILING DATE: 1999-03-26

PRIOR FILING DATE: 1999-03-26

PRIOR FILING DATE: 1999-03-26

NUMBER OF SEQ ID NOS: 43

SOFTWARE: PATENTIN VET: 2.1

FROM PRIOR DATE: 1999-03-26

NUMBER OF SEQ ID NOS: 43

FROM PRIOR DATE: 1999-03-26

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Description of Artificial Sequence:Rana
OTHER INFORMATION: catesbelana ribonuclease with (His)6 tag, Met at
OTHER INFORMATION: position 7, Met23Leu and Met58Leu substitutions
OTHER INFORMATION: (recombinant Met(-1) RaCOR1 Met27Leu Met57Leu-(His)6)
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98.3%; Score 591; DB 10; Length 117;
Best Local Similarity 98.2%; Pred. No. 2.7e-59;
Matches 107; Conservative 2; Mismatches 0; Indels (
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Pred. No. 2.7e-59;
2; Mismatches 0;
TITLE OF INVENTION: Recombinant Anti-Tumor RNase FILE REFERENCE: 015280-343110US
                                                       CURRENT APPLICATION NUMBER: US/09/948,391A
CURRENT FILING DATE: 2002-05-10
PRIOR APPLICATION NUMBER: US 60/079,751
PRIOR FILING DATE: 1998-03-27
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: W0 PCT/US99/06641
PRIOR APPLICATION NUMBER: US 09/622,613
PRIOR FILING DATE: 2000-08-17
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NOS: 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT ORGANISM: Artificial Sequence
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Best Local Similarity 98.2%;
Matches 107; Conservative
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ORGANISM: Rana catesbeiana
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US-09-961-400-22
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LENGTH: 111
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APPLICANT:
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OTHER INFORMATION: catesbeiana ribonuclease with Met at position 1
OTHER INFORMATION: (recombinant Met(-1) RaCOR1)
                                62 TTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
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98.3%; Score 591, DB 10; Length 111;
Best Local Similarity 99.1%; Pred. No. 2.5e-59;
Matches 108; Conservative 0; Mismatches 1; Indels
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APPLICANT: Newton, Dianne L.
APPLICANT: Newton, Dianne L.
APPLICANT: The United States of America
APPLICANT: as represented by The Secretary of the
APPLICANT: as represented by The Secretary of the
APPLICANT: Department of Health and Human Services
ITIED OF INVENTION: Recombinant Anti-Tumor Rhase
FILE REPRENCE: 015280-343110US
CURRENT APPLICATION NUMBER: US/09/948,391A
CURRENT FILING DATE: 1998-03-27
PRIOR PILING DATE: 1998-03-27
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 2000-08-17
NUMBER: OF SEQ ID NOS: 43
SOFTWARR: PAPELICATION NUMBER: US 09/622,613
NUMBER: OF SEQ ID NOS: 43
                                                                                                                                                                                                                                                                                     APPLICANT: Newton, Dianne L.
APPLICANT: The United States of America
APPLICANT: as represented by The Secretary of the
APPLICANT: Department of Health and Human Services
TITLE OF INVENTION: Recombinant Anti-Tumor RNase
FILE REFERENCE: 0152-80-3431110US
CURRENT PELLING DATE: 2002-05-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 6/079,751
PRIOR FILING DATE: 1998-03-27
PRIOR FILING DATE: 1998-03-26
PRIOR PILING DATE: 1999-03-26
PRIOR PILING DATE: 1999-03-26
PRIOR FILING DATE: 2000-08-17
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PATENTIN NOS: 43
SOFTWARE: PATENTIN NOS: 43
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                                                                                                                                                                               Sequence 17, Application US/09948391A Publication No. US20030027311A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                    APPLICANT: Rybak, Susanna M.
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US-09-961-400-21

Sequence 21, Application US/09961400

Publication No. US20030124131A1

GENERAL INFORMATION:
APPLICANT: RYBAK, SUSANNA M.
APPLICANT: GOLDENBERG, DAVID M.
APPLICANT: GOLDENBERG, DAVID M.
TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
TITLE OF INVENTION: CELLS
TITLE OF INVENTION: CELLS
TITLE OF INVENTION: UNMBER: US/09/961,400

CURRENT FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: 09/622,613
PRIOR PILING DATE: 1999-03-26
PRIOR PELING DATE: 1999-03-26
PRIOR FILING DATE: 1999-03-26
NUMBER OF SEQ ID NOS: 43

SOFTWARE PLANE PALELLY ON NUMBER: CO/079,751
PRIOR FILING DATE: 1999-03-26
NUMBER OF SEQ ID NOS: 43
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                                                                                                                                                                                                                                                                                                              Gaps
                                                                        OTHER INFORMATION: Description of Artificial Sequence:Rana OTHER INFORMATION: catesbeiana ribonuclease with Met at position 1, OTHER INFORMATION: Met23Leu and Met58Leu substitutions (recombinant OTHER INFORMATION: Met(-1) RaCOR1 Met22Leu Met57Leu)
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The United States of America
as represented by The Secretary of the
Department of Health and Human Services
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98.3%; Score 591; DB 10; 98.2%; Pred. No. 2.5e-59; iive 2; Mismatches 0;
                                                                                                                                                                                                                                                 98.3%; Score 591; DB 10;
98.2%; Pred. No. 2.5e-59;
iive 2; Mismatches 0;
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TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Rybak, Susanna M. APPLICANT: Newton, Dianne L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Rana catesbeiana
                                                                                                                                                                                                                                              Query Match 98.3
Best Local Similarity 98.2
Matches 107; Conservative
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Sequence 17, Application US/09961400
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US-09-961-400-19
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Publication No. US2033124131A1

Publication No. US2033124131A1

Publication No. US2033124131A1

APPLICANT: RYBAK, SUSANNA M.

APPLICANT: RYBAK, SUSANNA M.

APPLICANT: NEWTON, DIANNE L.

TITLE OF INVENTION: IMMUNOCONUUGATES OF TOXINS DIRECTED AGAINST MALIGNANT

TITLE OF INVENTION: IMMUNOCONUUGATES OF TOXINS DIRECTED AGAINST MALIGNANT

TITLE OF INVENTION: CELLS

CURRENT FILING DATE: 2001-09-25

PRIOR APPLICATION NUMBER: 09/622,613

PRIOR PILING DATE: 1999-03-26

PRIOR FILING DATE: 1999-03-26

PRIOR FILING DATE: 1998-03-26

NUMBER OF SEQ ID NOS: 43

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 15

LINGTH: 110
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                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Description of Artificial Sequence:Rana
OTHER INFORMATION: catesbeiana oocyte ribonuclease (RaCOR1) synthetic
OTHER INFORMATION: gene modified to use E. coli preferred codons
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Best Local Similarity 100.0%; Pred. No. 5.2e-60;
Matches 109; Conservative 0; Mismatches 0;
              PRIOR FILING DATE: 1998-03-27
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: WO PCT/US99/06641
PRIOR FILING DATE: 1999-03-26
PRIOR APPLICATION NUMBER: US 09/622,613
PRIOR FILING DATE: 2000-08-17
NUMBER OF SEQ ID NOS: 43
SEQ ID NO 15
PRIOR APPLICATION NUMBER: US 60/079,751
                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence
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ORGANISM: Rana catesbeiana
US-09-961-400-15
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US-09-961-400-15
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RESULT 7 US-09-961-400-17

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APPLICANT: STRAK, SUSANNA M.
APPLICANT: GOLDENBERG, DAVID M.
APPLICANT: GOLDENBERG, DAVID M.
TITLE OF INVENTION: IMMUNOCONUUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
TITLE OF INVENTION: CELLS
TITLE OF INVENTION: CELLS
TITLE OF INVENTION: USANDER: US/09/961,400
CURRENT APPLICATION NUMBER: 09/622,613
FRIOR FILING DATE: 2001-09-25
FRIOR PRILING DATE: 2000-00-17
PRIOR APPLICATION NUMBER: 09/622,613
FRIOR PRILING DATE: 1999-03-26
FRIOR FILING DATE: 1999-03-26
FRIOR FILING DATE: 1998-03-26
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PARCHILIN Ver. 2.1
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| Publication No. US20030124131A1
| Publication No. US20030124131A1
| APPLICANT: RYBAK, SUSANNA M. | APPLICANT: RYBAK, SUSANNA M. | APPLICANT: COLDENBERG, DAVID M. | APPLICANT: ROLDENBERG, DAVID M. | APPLICANT: NEWTON, DIANNE L. | TITLE OF INVENTION: CELLS | TITLE OF INVENTION: CELLS | FILE REFERENCE: 018733/1059 | CURRENT APPLICATION NUMBER: US/09/961,400 | FRIOR APPLICATION NUMBER: 09/622,613 | PRIOR APPLICATION NUMBER: O9/622,613 | PRIOR APPLICATION NUMBER: PCT/US99/06641 | PRIOR APPLICATION NUMBER: PCT/US99/06641 | PRIOR FILING DATE: 1998-03-26 | PRIOR FILING DATE: 1998-03-26 | PRIOR FILING DATE: 1998-03-26 | PRIOR FILING DATE: 1998-03-26 | PRIOR FILING DATE: 1998-03-26 | PRIOR FILING DATE: 1998-03-26 | PRIOR FILING DATE: 1998-03-26 | PRIOR FILING DATE: 1998-03-26 | PRIOR FILING DATE: 1998-03-26 | PRIOR FILING DATE: 1998-03-26 | PRIOR FILING DATE: 1998-03-26 | PRIOR FILING DATE: 1998-03-26 | PRIOR FILING DATE: 1998-03-26 | PRIOR FILING DATE: 1998-03-26 | PRIOR FILING DATE: 1998-03-26 | PRIOR FILING DATE: 1998-03-26 | PRIOR FILING DATE: 1998-03-26 | PRIOR FILING DATE: 1998-03-26 | PRIOR FILING DATE: 1998-03-26 | PRIOR FILING DATE: 1998-03-26 | PRIOR FILING DATE: 1998-03-26 | PRIOR FILING DATE: 1998-03-26 | PRIOR FILING DATE: 1998-03-26 | PRIOR FILING DATE: 1998-03-26 | PRIOR FILING DATE: 1998-03-26 | PRIOR FILING DATE: 1998-03-26 | PRIOR FILING DATE: 1998-03-26 | PRIOR FILING DATE: 1998-03-26 | PRIOR FILING DATE: 1998-03-26 | PRIOR FILING DATE: 1998-03-26 | PRIOR FILING DATE: 1998-03-26 | PRIOR FILING DATE: 1998-03-26 | PRIOR FILING DATE: 1998-03-26 | PRIOR FILING DATE: 1998-03-26 | PRIOR FILING DATE: 1998-03-26 | PRIOR FILING DATE: 1998-03-26 | PRIOR FILING DATE: 1998-03-26 | PRIOR FILING DATE: 1998-03-26 | PRIOR FILING DATE: 1998-03-26 | PRIOR FILING DATE: 1998-03-26 | PRIOR FILING DATE: 1998-03-26 | PRIOR FILING DATE: 1998-03-26 | PRIOR FILING DATE: 1998-03-26 | PRIOR FILING DATE: 1998-03-26 | PRIOR FILING DATE: 1998-03-26 | PRIOR FILING DATE: 1998-03-26 | PRIOR FILING
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Publication No. US20030124131A1
GENERAL INFORMATION:
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ORGANISM: Rana catesbeiana
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SOFTWARE: PatentIn Ver. 2.1
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                                                                                                                                                                                             Sequence 44, Application US/09961400

publication No. US20030124131A1

publication No. US20030124131A1

publication No. US20030124131A1

APPLICANT: RYBAK, SUSANNA M.

APPLICANT: GOLDENBERG, DAVID M.

APPLICANT: NEWTON, DIANNE L.

TITLE OF INVENTION: CELLS

FILE REFERENCE: 018733/1059

CURRENT APPLICATION NUMBER: US/09/961,400

CURRENT APPLICATION NUMBER: 09/622,613

PRIOR PAPLICATION NUMBER: 09/622,613

PRIOR PLING DATE: 2000-08-17

PRIOR PLING DATE: 1999-03-26

PRIOR PLING DATE: 1999-03-26

PRIOR PLING DATE: 1998-03-26

SOFTWARE: PatentIN Ver. 2.1

SEQ ID NO 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 SNWATFQOKHIINTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNVL 60
SNWATFQQKHIINTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNVL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 SNWATFOOKHIINTPIICNTIMDNNIYIVGGOCKRVNTFIISSATTVKAICTGVINMNVL
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Pred. No. 1.8e-60;
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APPLICANT: Newton, Dianne L.
APPLICANT: Newton, Dianne L.
APPLICANT: The United States of America
APPLICANT: The United States of America
APPLICANT: Department of Health and Human Services
TITLE OF INVENTION: Recombinant Anti-Tumor Rnase
FILE REFERENCE: 015280-34311005
CURRENT APPLICATION NUMBER: US/09/948,391A
CURRENT APPLICATION NUMBER: US 00/079,751
PRIOR APPLICATION NUMBER: WO PCT/US99/06641
PRIOR FILING DATE: 1998-03-26
PRIOR FILING DATE: 1998-03-26
PRIOR FILING DATE: 1998-03-26
PRIOR FILING DATE: 1098-03-26
PRIOR FILING DATE: 1098-03-26
PRIOR FILING DATE: 1098-03-26
PRIOR FILING DATE: 1098-03-26
PRIOR FILING DATE: 2000-08-17
SEQ ID NO SEQ ID NOS: 43
ILENGTH: 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Rana catesbelana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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Best Local Similarity
Matches 110; Conserv
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US-09-948-391A-26
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APPLICANT: RYBAK, SUSANNA M.
APPLICANT: GOLDENBERG, DAVID M.
APPLICANT: GOLDENBERG, DAVID M.
TAPLICANT: GOLDENBERG, DAVID M.
TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
TITLE OF INVENTION: CELLS
TITLE OF INVENTION: CELLS
FILE REPERENCE: 104731/1059
CURRENT APPLICATION NUMBER: US/09/961,400
CURRENT FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: 09/622,613
PRIOR APPLICATION NUMBER: 09/6241
PRIOR PILING DATE: 1999-03-26
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 1999-03-26
NUMBER OF SEQ ID NOS: 43
SOPTWARE: Patentin Ver. 2.1
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                                                                                                                                                                                                                                     Gaps
OTHER INFORMATION: Description of Artificial Sequence: Rana OTHER INFORMATION: catesbeiana ribonuclease with Met at position 1: OTHER INFORMATION: and Gln2Ser substitution (Met (-1) RacOR1 Q1S) US-03-948-91A-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 STTREQLATCTRISITPRPCPYSSRIEINYICVKCENQYPVHFAGIGRCP 111
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                                                                                                                                                                    Length 111;
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APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: The United States of America
APPLICANT: as represented by The Secretary of the
APPLICANT: Department of Health and Human Services
TITLE OF INVENTION: Recombinant Anti-Tumor RNase
FILER REFERENCE: 015280-343110US
CURRENT APPLICATION UNMBER: US/09/948,391A
                                                                                                                                                                100.0%; Score 601; DB 10;
100.0%; Pred. No. 1.8e-60;
tive 0; Mismatches 0;
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US-09-961-400-26
Sequence 26, Application US/09961400
Superioration No. US20030124131A1
GENERAL INFORMATION:
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Matches 110; Conservative
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May 11, 2004, 14:34:38; Search time 37.8281 Seconds (without alignments) 807.135 Million cell updates/sec
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1 SNWATFQQKHIINTPIICNT.....ICVKCENQYPVHFAGIGRCP 110
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1. (cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

2. (cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

2. (cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*

2. (cgn2_6/ptodata/2/pubpaa/DSO8_NEW_PUB.pep:*

3. (cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*

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3. (cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

4. (cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

4. (cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*

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4. (cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*

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6. (cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*

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6. (cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

6. (cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Sequence 24, Appl	Sequence 24, Appl	Sequence 26, Appl	Sequence 26, Appl	15,	Sequence 15, Appl	Sequence 17, Appl	19,	Sequence 17, Appl	Sequence 21, Appl	Sequence 21, Appl	Sequence 22, Appl	Sequence 22, Appl	Sequence 19, Appl	Sequence 11, Appl
SUMMARIES	ΩI	US-09-948-391A-24	US-09-961-400-24	US-09-948-391A-26	US-09-961-400-26	US-09-948-391A-15	US-09-961-400-15	US-09-961-400-17	US-09-961-400-19	US-09-948-391A-17	US-09-948-391A-21	US-09-961-400-21	US-09-948-391A-22	US-09-961-400-22	US-09-948-391A-19	US-09-948-391A-11
		10	10	10	10	10	10	10	10	10	10	10	10	10	10	10
	Query Match Length DB	110	110	111	111	110	110	111	110	111	111	111	117	1117	110	104
o k o	Query Match	100.0	100.0	100.0	100.0	99.3	99.3	99.3	98.3	98.3	98.3	98.3	98.3	98.3	97.3	46.7
	Score	601	601	601	109	597	597	597	591	591	591	591	591	591	585	280.5
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US-09-961-400-11 US-09-948-391A-13	US-09-961-400-13	US-09-961-400-2	US-09-948-391A-6	US-09-961-400-6	US-09-948-391A-28	US-09-961-400-28	US-09-948-391A-2	US-09-961-400-9	US-09-986-119-1	US-09-918-887-1	US-10-153-882-2	US-09-948-391A-4	US-09-961-400-4	US-09-961-400-8	US-10-461-713-53	US-09-948-391A-8	US-09-948-391A-9	US-09-986-119-3	US-09-918-887-3	US-10-016-447-2	US-10-037-417-103	US-10-016-248-89	US-10-074-978A-139	US-10-074-978A-141	US-10-461-713-52	872-25	US-09-876-997-254	US-09-981-286A-8
10	10	10	10	10	10	10	10	10	σ	70	14	10	10	10	12	10	10	6	10	13	12	12	15	15	12	6	10	σ
104	105	104	105	105	127	127	104	111	104	104	105	104	104	105	104	105	111	83	83	169	124	119	119	66	124	147	147	124
46.7	46.7	46.0	46.0	46.0	46.0	46.0	45.8	45.5	45.3	45.3	45.3	45.0	45.0	45.0	44.0	43.5	43.5	34.3	34.3	26.3	22.5	21.0	21.0	20.1	19.6	19.5	19.5	19,1
280.5	280.5	276.5	276.5	276.5	276.5	276.5	275.5	273.5	272.5	272.5	272.5	270.5	270.5	270.5	264.5	261.5	261.5	206	206	158	135.5	126.5	126.5	121	117.5	117	117	114.5
16	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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Sequence 24, Application US/09948391A

Sequence 24, Application US/09948391A

Publication No. US20030027311A1

GENERAL INFORMATION:

APPLICANT: Rybak, Susanna M.

APPLICANT: Rybak, Dianne L.

APPLICANT: The United States of America

APPLICANT: The United States of America

APPLICANT: Department of Health and Human Services

TITLE OF INVENTION: Recombinant Anti-Tumor RNase

FILE REFERENCE: 015280-34310US

CURRENT APPLICATION NUMBER: US 60/079,751

PRIOR APPLICATION NUMBER: US 60/079,751

PRIOR APPLICATION NUMBER: US 60/079,751

PRIOR FILING DATE: 1999-03-26

PRIOR FILING DATE: 1999-03-26

PRIOR FILING DATE: 1999-03-26

PRIOR FILING DATE: 1999-03-26

PRIOR FILING DATE: 1999-03-26

PRIOR FILING DATE: 1099-03-26

PRIOR APPLICATION NUMBER: US 60/079,751

PRIOR FILING DATE: 1099-03-26

PRIOR FILING DATE: 1099-03-26

PRIOR APPLICATION NUMBER: US 60/079,751

PRIOR FILING DATE: 1090-03-26

JOHNER PRIOR MATION: Catesbelana ribonuclease with Giniber substitution OTHER INFORMATION: Catesbelana ribonuclease with Giniber substitution OTHER INFORMATION: Catesbelana ribonuclease with Giniber substitution US-09-949-391A-24

OTHER INFORMATION: Catesbelana ribonuclease with Giniber substitution US-09-949-391A-24

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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae, Colobinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 QDWLTFQKKHLTNT----RDVDCNNIMSTN--LFHCKDKNTFIYSRPEPVKAIC---KGI
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Pygathrix bieti (Black snub-nosed monkey) (Rhinopithecus bieti).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae; Colobinae;
Pygathrix.
NCBI_TaxID=61621;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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MEDLINE=22597544; PubMed=12711394;
Zhang J., Zhang Y.-F.;
"Pseudogenization of the tumor-growth promoter angiogenin in a leaf-
                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=22597544; PubMed=12711394;
Zhang J., Zhang Y.-P.;
"Pseudogenization of the tumor-growth promoter angiogenin in a leaf-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22.4%; Score 129.5; DB 6; Length 146; 34.2%; Pred. No. 4.1e-07; ive 16; Mismatches 40; Indels 17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         eating monkey.";
Gene 308:95-101(2003).
Gene 308:95-101(2003).
EMBL, AY221130; AA041337.1; -.
EMBL, AY221130; AA041337.1; -.
GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
R GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
R IPROPATOR PROMASEA.
R PÉRM: PROMO74; RIABONUCLEASE.
R PRODOR; PROMO55; RNASeB.
R PROSITE; PROMO52; RNASEB PANCREATIC; 1.
R PROSITE; PSOM127; RNASE PANCREATIC; 1.
R PROSITE; PSOM127; RNASE PANCREATIC; 1.
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Gene 308:95-101(2003).

EMBL, AY221131; AA041338.1;

GO, GO:0003676; Finucleic acid binding; IEA.

GO; GO:0004522; Fipancreatic ribonuclease activity; IEA.

InterPro; IPR001427; RNaseA.
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PRINTS; PR00794; RIBONUCLEASE.
ProDom: PD000535; RNaseA; 1.
SMART; SM00092; RNASE PC; 1.
PROSITE; PS00127; RNASE PC; 1.
SEQUENCE 146 AA; 16438 MW; 8CF170A4BD12BA67 CRC64;
                                                                                    01-07N-2003 (TrEMBLrel. 24, Created)
01-07N-2003 (TrEMBLrel. 24, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
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Last annotation update)
                                        146 AA
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                                        PRT;
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Best Local Similarity 34.2*,
Thes 38; Conservative 7
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                                     PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=61622;
                                                                                                                                                                                    Angiogenin.
Q861Y3
D0 Q861X3;
DT O1-JUN;
DT O1-JUN;
DE Angiogen
OS Pygathm;
OC Bukaryol
OC Mamalyi
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Q861Y2
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                                                              1 QDWLTFQKKHLTNT----RDVDCNNIMSTN--LFHCKDKNTFIYSRPEPVKAIC---KGI
                           Gaps
                                                                                                            52 IASKNV-LTTSEFYLSDCNV---TSR-PCKYKLKKSTNTFCVTCENQAPVH 97
                          17;
   Length 146;
                          Indels
   DB 6;
                         40;
22.4%; Score 129.5; DB 6
34.2%; Pred. No. 4.1e-07;
iive 16; Mismatches 40
                         Conservative
 Query Match
Best Local Similarity
Matches 38; Conserv
                       38;
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Search completed: May 7, 2004, 21:46:01 Job time : 31.5753 secs 2

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EMBL; AF159166; AAD41901.1; -. HSSP; P00656; 1LSQ.
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01-NOV-1999 (TrEMBLrel. 12,
01-OCT-2003 (TrEMBLrel. 25,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FRL2 protein.
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01-NOV-1999
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Q9W738
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23 QDWPTFQQKHIPSTSSIDCNTIMDKDIYIVRGQCKKVNTFIIYSATTVKAICTGVLNS-N 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.; Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF288642, AAG30414.2; -.
HSSP; Pl1916, 1BC4.
GO; GO:0003676; F:nucleic acid binding; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                   MEDLINE=21539506; PubMed=11683320;
Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
"Rapid diversification of RNase A superfamily ribonuclease from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana,
NCBI_TaxID=8400;
                                                                                                                                                                                                     Bukaryota; Metazoa; Chordača; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana
NCBI_TaxID=8400;
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Liao Y.D., Huang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.C.;
Purification and cloning of cytotoxic ribonucleases from Rana catesbeiana (bullfrog) ";
Nucleic Acids Res. 28:4097-4104 (2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  82 VLSTTREQLXXXTRTFITSRPCPYSSTKETNKICVKCENEYPVHFAGIGKC 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57 VLTTSEFYLSDCN---VTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35; Indels
                                                                                                                                                                                                                                                                                                                                                                                    bullfrog, Rana catesbelana.";
J. Mol. Evol. 53:31-38(2001).

BNBL; AF351208; AK30254.1;
HSSP; P11916; 1BC4.
GO; GO:0003576; F:nucleic acid binding; IEA.
GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
InterPro; IRR001427; RNaseA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIĞNAL 1 22 POTENTIAL.
SEQUENCE 132 AA; 14704 MW; 95D61760F729868E CRC64;
                                                                                 01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 25, Last annotation update)
RNase A-type ribonuclease rc204 precursor.
Rana catesbeiana (Bull frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2001 (TrEMBLrel. 16, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
RC-RNasell ribonuclease precursor.
Rana castesbeiana (Bull frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       48.4%; Score 280; DB 13;
48.6%; Pred. No. 1.3e-24;
ative 14; Mismatches 35;
                                             132 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00074; rnaséA; 1.
ProDom; PD000535; RnaseA; 1.
SMART; SM00092; RNASe Pc; 1.
PROSITE; PS00127; RNASE PANCREATIC; 1.
                                        PRT;
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                                           PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
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SIGNAL
                                                              Q98SM1;
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                                           CMS860
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33 FMEKHIVKEGAETNCNQTIKDRNIRFKN--NCKFRNTFIHDTNGKKVKEMCAGIVKSTFV 90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22 QNWAKFKEKHITSTSSIDCNTIMDKAIYIVGGKCKERNTFIISSEDNVKAICSGVSPDRK 81
                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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"The identification of two novel ligands of the FGF receptor by a yeast screening method and their activity in Xenopus development."; Cell 83:621-630(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57 VLTTSEFYLSDC---NVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
                                                                                                                                                                                                                                                                                                                                                                                                                       7;
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                                                                                                                                                                                                                                                                                                                                                             DB 13; Length 132;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        / Match 27.2%; Score 157.5; DB 13; Length Local Similarity 36.1%; Pred. No. 2.7e-10; Seconservative 19; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                          Query Match 47.7%; Score 275.5; DB 13; Length Best Local Similarity 44.1%; Pred. No. 4.3e-24; Matches 49; Conservative 19; Mismatches 36; Indels
GG, GO:0004522; F:pancreatic ribonuclease activity; IEA. InterPro; IPR001427; RNaseA. Pfam; PF00074; rnaseA. 1. Proport; PD000535; RNaseA. 1. SMART; SM00053; RNASEA PC; 1. PROSITE; PS00127; RNASE_PROREATIC; 1.
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Kinoshita N., Kirschner M.W.;
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
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GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
InterPro; IFROM 1877; RNASEA.
ProDom; PD000535; RNASEA; 1.
PROSITE; PS00127; RNASE PANTEATIC; 1.
SEQUENCE 169 AA; 18891 MW; D969F3E43B3CE1B8 CRC64;
                                                                                                                                                                                                                              1 21 POTENTIAL.
22 132 RC-RNASEL1 RIBONUCLEASE.
132 AA; 14625 MW; D8D9AS17452FBE53 CRC64;
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Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Xenopus laevis (African clawed frog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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EMBL; AF351207; AAK30253.1; -. EMBL; AF359578; AAL87036.1; -. HSSP; P11916; 1BC4.
                                                                                                                                                       132 AA;
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                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=8400;
                                                                                                                                  1 23
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01-JUN-2001
                                                                                                                                                                                                    53;
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                                                                                                                                                       SEQUENCE
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                                                                                                                      Signal.
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                                                                                                                                  SIGNAL
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Q98SL8
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23 QNWATFQQKHITNTSSINCSNIMNNSLYIVGGQCKKVNTFIASSATTVKGICSG-VTDKK 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                              SEQUENCE FROM N.A.

MEDLINE=2139506; PubMed=11683320;
Rosenberg H.F., Zhang U., Liao Y.-D., Dyer K.D.;

"Rapid diversification of Riase A superfamily ribonuclease from the bullfrog, Rana catesbeiana.";

U. MOL. EVOL. 53.31-38(2001).

EMBL; AF351210; AAK30256.1; -.

HSSP; P11916; 1BC4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=21539506; PubMed=11683320;
Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
"Rapid diversification of RNase A superfamily ribonuclease from the bullfrog, Rana ctesbeiana.";
J. Mol. Evol. 53:31-38(2001).
                                                                                       01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 15, Last annotation update)
RNase A-type ribonuclease rc212 precursor.
Rana catesbeiana (Bull frog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Neobatrachia, Ranoidea, Ranidae, Rana
82 VLSTIRRQLNICTRISIIPRPCPYSSRIENNYICVKCENQYPVHFAGIGRC 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57 VLTTSEFYLSDCN---VTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OT-2003 (TrEMBLrel. 25, Last annotation update)
RNASe A-type ribonuclease rc203 precursor (RC-RNase7 precursor).
Rana catesbeiana (Bull frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                    8
                                                                                                                                                                                                                                                                                                                                                                                                                           Length 133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Liver;
Liao Y.-D., Tang P.-C., Jeng J.-T.;
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                          GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
InterPro; IPR001427; RNaseA.
                                                                                                                                                                                                                                                                                                                                                                                       SIGNAL 1 22 POTENTIAL.
SEQUENCE 133 AA; 14615 MW; C8785B236B26E54E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                        49.5%; Score 286; DB 13; 47.7%; Pred. No. 2.6e-25;
                                                                      133 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                17; Mismatches
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                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                         ProDom; PD000535; RNaseA; 1.
SMART; SM00092; RNASe Pc; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                53; Conservative
                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                           Pfam; PF00074; rnaseA; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
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                                                                                                                                                                          NCBI TaxID=8400;
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                                                                                 Q98SL9;
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                                                                    Q98SL9
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Q98SM2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ODWLIFOKKHLINIRDVDCNNIMSINLF----HCKDKNIFIYSRPEPVKAICKGIIASKN 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23 QNWATFQEQHITNISSINCSNIMNNSLYIVGGQCKKVNTFIASSATTVKGICSG-VIDKK 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 QDWLTFQKKHLTNTRDVDCNNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=21539506; PubMed=11683320;
Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
"Rapid diversification of RNase A superfamily ribonuclease from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ana catebbelana (M11 1709).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Amphibia, Batrachia, Anura, Neobatrachia, Ranoidea, Ranidae, Rana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82 VLSSTKFQLDICTRIFITPRPCPYSSRTETNYICVKCENQYPVHFAGIGQC 132
                                                                                                                                                                                                                                                                                                                                                                                                       8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57 VLTTSEFYLSDC---NVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ch 48.8%; Score 282; DB 13; Length 133; l Similarity 46.8%; Pred. No. 7.7e-25; 52; Conservative 18; Mismatches 33; Indels
                                                                                                                                                                                                                                                                                                                                               Length 132;
                                                                                                                                                                                                                                                                                                                                                                                                       Indels
GO, GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
InterPro; IPR001427; RNaseA.
Pfam; PF00074; rnaseA; 1.
ProDom; PD000535; RNaseA; 1.
SMART; SM00092; RNASE PC; 1.
PROSITE; PS00127; RNASE_PC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    bullfrog, Rana catesbelana.";
J. Mol. Evol. 53:31-38(2001).
BMBL; AF351211; AK30257.1; -.
HSSP; P1191: 1BC4
GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
InterPro; IPR001427; RNaseA.
                                                                                                                                                                                                                                                          132 RC-RNASE7.
14412 MW; 131A745187978687 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-2001 (TrEMBLrel. 17, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) RNase A-type ribonuclease rc218 precursor. Rana catesbeiana (Bull frog).
                                                                                                                                                                                                                                                                                                                                         49.3%; Score 285; DB 13; I
47.7%; Pred. No. 3.4e-25;
tive 14; Mismatches 36;
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                                                                                                                                                                                                                                   POTENTIAL.
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ProDom; PD000535; RnaseA; 1.
SMART; SM00092; RNASe Pc; 1.
PROSITE; PS00127; RNASE_PANCREATIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL
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14590 MW;
                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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132
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1 QDWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT 60
                                                                                         Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.; Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24 ODWDTFQKKHLIDTKKVKCDVEMKKALFDCKKINTFIFARPPRVQALCKNIKDNINVLSR
                                                                                                                                                                                                                                                                                                                                                                                                                            Length 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 SEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84 DVFYLPQCNRKKLPCHYRLDGSTNTICLTCMKELPIHFAGVGKC 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                            aumillocal (MOG-ZOI) (U. The Embil Gelibalik) Dibo databases.
EMBI, AFE42556; AAG31442.2; -1.
HSSP; P22069; IONC.
GO; GO:0003676; P:moleic acid binding; IEA.
InterPro; IPR001427; RNaseA.
Pfam; PF00074; TnaseA.
Probom; P10000535; RNaseA.
PROSITE; PS00127; RNASEA.
                                                                                                                                                                                                                                                                                                                                                                                14804 MW; AFEBFD67D266C7C2 CRC64;
                                                                                                                                                                                                                                                                                                                                                            RC-RNASE6 RIBONUCLEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35;
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49.5%; Pred. No. 1.1e-26;
ive 16; Mismatches 32;
                                                                                                                                                                                                                                                                                                                                                                                                                            DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                                          ch 53.5%; Score 309; DB 13; 1 Similarity 53.8%; Pred. No. 5.4e-28; 56; Conservative 13; Mismatches 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 133 AA
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    Nucleic Acids Res. 28:4097-4104(2000)
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Matches 55; Conservative
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24 1
128 AA;
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SIGNAL
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24 QNWETFQKKHLIDTRDVKCDAEMKKALFDCKQKNTFIYARPGRVQALCKNIIVSKNVLST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                       01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
RC-RNasea ribonuclease precursor.
Rana catesbeiana if frog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia; Batrachia, Anura; Neobatrachia, Ranoidea; Rana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Euteleostomi;
Ranidae; Rana
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MEDLINE=20512555; PubMed=11058105;
Liao Y.D., Huang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.C.;
"Purification and cloning of cytotoxic ribonucleases from Rana catesbeiana (bullfrog).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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"Purification and cloning of cytotoxic ribonucleases from Rana catesbeiana (bullfrog).";
Nucleic Acids Res. 28:4097-4104 (2000).
EMBL; AF242554; AAG31440.2; ---
HSSP; P22069; 10NC.
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                                                                  SEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
                                                                                         35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 SEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84 DAFLLPQCDRIKLPCHYKLSSSTWTICITCVNQLPIHFAGVGSC 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
InterPro; IPR001427; RNaseA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RC-RNASE3 RIBONUCLEASE.
2B14986082E0587D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2001 (TrEMBLrel. 16, Created)
01-0CT-2001 (TrEMBLrel. 18, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
RC-RNase6 ribonuclease precursor.
Buran catesbeiana (Bull frog).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   53.8%; Score 311; DB 13;
54.8%; Pred. No. 3.2e-28;
                                                                                                                                                                                                                             128 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          128 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00074; rnaseA; 1.
ProDom; PD000535; RNaseA; 1.
PROSITE; PS00127; RNASE_PANCREATIC; 1.
                                                                                                                                                                                                                                                                      01-MAR-2001 (TrEMBLrel. 16, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Liver;
MEDLINE=20512555; PubMed=11058105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14517 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1
24 1
128 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=8400;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=8400;
                                                                     61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9DFY5
                                                                                                                                                                                                                           Q9DFY7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Signal
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                                                                                                                                                                               RESULT 5
                                                                                                                                                                                                      O9DFY7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11 SEQUENCE FROM N.A.

12 SEQUENCE FROM N.A.

13 MEDLINE=21539506; PubMed=11683320;

14 Rosenberg H.E., Zhang J., Liao Y.-D., Dyer K.D.;

15 Rosenberg H.E., Zhang J., Liao Y.-D., Dyer K.D.;

16 The persification of RNase A superfamily ribonuclease from the control of RNase A superfamily ribonuclease from the large of Rosenberg Radio actesbeiana...;

16 J. Mol. Evol. 53:31-38(2001).

17 Mol. Evol. 53:31-38(2001).

18 MSSP; P11916; 1824.

19 ROSP; P11916; 1824.

19 ROSP; P11916; 1824.

10 ROJ GO:0003676; Funcleic acid binding; IEA.

10 ROJ GO:0004522; Fipancreatic ribonuclease activity; IEA.

18 Probom; P0000535; RNaseA.

19 Robom; P0000535; RNaseA.

10 Robom; P0000535; RNaseA.

10 Robom; P0000535; RNaseA.

10 Robom; P0000535; RNaseA.

10 Robom; P0000535; RNaseA.

11 Robom; P0000535; RNaseA.

12 Robom; P0000535; RNaseA.

13 Robom; P0000535; RNaseA.

14 Robom; P0000535; RNaseA.

15 ROBOM; P0000535; RNaseA.

16 Robom; P0000535; RNaseA.

17 Robom; P0000535; RNaseA.

18 Robom; P0000535; RNaseA.

18 Robom; P0000535; RNaseA.

18 Robom; P0000535; RNaseA.

18 Robom; P0000535; RNaseA.

18 Robom; P0000535; RNaseA.

18 Robom; P0000535; RNaseA.

18 Robom; P0000535; RNaseA.

18 Robom; P0000535; RNaseA.

18 Robom; P0000535; RNaseA.

18 Robom; P0000535; RNaseA.

18 Robom; P0000535; RNaseA.

18 Robom; P0000535; RNaseA.

18 Robom; P0000535; RNaseA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8; Gaps
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-CUT-2003 (TrEMBLrel. 25, Last annotation update)
RNase A-type ribonuclease rc208 precursor.
Rana catesbeiana (Bull frog).
Ruhar catesbeiana (Bull frog).
Amphibia; Batrachia; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Ranidae; Rana NCBL TaxID=8400;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57 VLTTSEFYLSDC---NVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22 POTENTIAL.
14628 MW; 87FCF122C3499E02 CRC64;
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24 ODWATFKKKHLTDTWDVDCDNLMPTSLFDCKDKNTFIYSLPGFVKALCRGVIFSADVLSN 83
                                                              P.-C., Wang S.-C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P.-C., Wang S.-C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 QDWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ODWLIFOKKHLINTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2003 (TrEMBLrel. 15, Last annotation update)
RO-GCT-2003 (TrEMBLrel. 25, Last annotation update)
RC-RNase2 ribonclease precursor.
Rana catesbeiana (Bull frog).
Rana catesbeiana (Bull frog).
Rana catesbeiana (Antaraca, Craniata, Vertebrata, Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Rancidea; Ranidae; Rana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Liao Y.D., Huang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.C., "Purification and cloning of cytotoxic ribonucleases from Rana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 13; Length 129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         66.8%; Score 386; DB 13; Length 128; 67.3%; Pred. No. 6.4e-37; ive 10; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-Liver;
ILISOUE-Liver;
Lidao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C.,
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AF24253; AAG31439.1; --
PDB, 1MS8; 09-JMN-03.
ROG, GO:0003676; F:nucleic acid binding; IEA.
ROG, GO:0004522; F:panoreatic ribonuclease activity; IEA.
InterPro; IPR001427; RNaseA.
Probom; PD00074; rnaseA.
Probom; PR00074; rnaseA.
PROSITE; PS00127; RNASE_PANCREATIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84 SEFYLAECNVKPRXPCKYKLKKSSNRICIRCEHELPVHFAGVGIC 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 SEFYLSDCNVTSR-PCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    70.0%; Score 404.5; DB 13; Length 67.6%; Pred. No. 4.6e-39; ive 16; Mismatches 17; Indels
                                                   Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C. Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases. BNBL, AF242555, AAG31441.2; -. BNBL, AF242555, AAG31441.2; -. BNBL, IKW2: 2-6-ULL-O. 2-6-ULL-O. 3-6-ULL-O.                                                                                                                                                                                                                                                                                                                                                                                                                    826A62882B10ABDA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RC-RNASE2 RIBONUCLEASE.
989719CF52053ECC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                             RC-RNASE4 RIBONUCLEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                              POTENTIAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=20512555; PubMed=11058105;
                                                                                                                                                                                                                                                                                                                                                                                                                 129 AA; 14724 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             71; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              catesbeiana (bullfrog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      128 AA;
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        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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SIGNAL
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24 QDWLTFQKKHITNTRDVDCDNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 QDWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Neobatrachia, Ranoidea, Ranidae, Rana.
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Amphibia, Batrachia, Anura, Neobatrachia, Ranoidea, Ranidae, Rana.
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Nucleic Acids Res. 28:4097-4104(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEFYLSDCNVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 127
                                                                                     SEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lido Y.-D., Wang S.-C.;
"Rana pipiens onconase genomic DNA.";
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AF32139; AAL541383.1;
-PIK; A39035, A39035.
GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        953F90D351CFEEF3 CRC64;
                                                                                                                    SEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC
                                                                                                                                                                                                                                                                                                                              01-WAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2001 (TrEMBLrel. 16, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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PROSITE; PS00127; RNASE PANCREATIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rana pipiens (Northern leopard frog).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=20512555; PubMed=11058105;
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SEQUENCE 127 AA; 14469 MW;
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ProDom; PD000535; RNaseA; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                 Onconase precursor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=8404;
                                                                                     19
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SIGNAL
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ID 209FY7
AC 29DF 01-00
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

7, 2004, 21:29:10 ; Search time 29.5753 Seconds (without alignments) 1109.503 Million cell updates/sec Мау Run on:

US-09-961-400-2 578 1 QDWLTFQKKHLTNTRDVDCM.....TFCVTCENQAPVHFVGVGHC 104 Title: Perfect score:

Sequence:

Scoring table:

Searched:

BLOSUM62 Gapop 10.0 , Gapext 0.5

1017041 Total number of hits satisfying chosen parameters:

1017041 seqs, 315518202 residues

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SPTREMBL 25:* Database :

sparchea:*
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spbacteria:*
sp fund:*
sp invertebrate:*
sp mhc:*
sp organal:*
sp phage:*
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sp vertebrate:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

					SUMMARIES	
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Result		Query				
No.	Score	Match	tore Match Length DB I	DB	QI	Description
٦	578	100.0	127	13	918V8	O9i8v8 rana pipien
7	556	96.2	127	13	QBUVXS	OBuvx5 rana pipien
m	404.5	70.0	129	13	Q9DFY6	Ogdfv6 rana catesh
4	386	8.99	128	13	Q9DFY8	09dfv8 rana catesb
N	311	53.8	128	13	O9DFY7	Ogdfv7 rana catesb
9	309	53.5	128	13	Q9DFY5	Ogdfv5 rana catesb
7	298	51.6	133	13	098SM0	O98sm0 rana catesb
80	286	49.5	133	13	Q98SL9	098819 rana catesb
σ	285	49.3	132	13	098SM2	098sm2 rana catesb
10	282	48.8	133	13	Q98SL8	098s18 rana catesb
11	280	48.4	132	13	Q98SM1	098sml rana catesb
12	275.5	47.7	132	13	Q9DF78	09df78 rana catesb
13	157.5	27.2	169	13	Q9W738	09w738 xenopus lae
14	129.5	22.4	146	ø	Q861Y3	0861v3 pygathrix r
15	129.5	22.4	146	9	Q861Y2	0861v2 pygathrix b
16	129.5	22.4	146	9	0861Y1	O861v1 pvgathrix a

Q9jki5 mus saxicol Q9jki9 meriones un Q9jki7 mus saxicol Q9jkj3 meriones un Q861y4 trachypithe	O9jkj4 meriones un O9jkj4 mus saxicol O9jkj1 meriones un O7yrj6 balaena mys O9jkj2 meriones un	29jki3 mus panati Q9jki3 mus saxicol Q7yrj5 tursiops tr Q9jki6 mus saxicol Q9tv25 eulemur ful Q9jki2 mus saxicol	V91X14 mus saxicol Q861y5 colobus que Q9bec1 tragulus ja Q9tsq6 cercopithec Q9tv32 gorilla gor Q9tv24 galago moho Q8hzq0 pan troqlod	Q9r134 rattus norv Q9jkg6 mus caroli Q9jkh7 mus caroli Q9tv30 saguinus oe Q9r125 mus musculu Q9jkh8 mus pahari
11111			146 6 0861YS 170 6 09BEC1 170 6 09BEC1 119 6 09TYS0 132 6 09TY24 147 6 08HZQ0	155 11 Q9K134 156 11 Q9JKG6 156 11 Q9JKH7 119 6 Q9TY30 155 11 Q9K125 155 11 Q9KH8
22.3 22.0 21.9 21.8	21.3 21.3 20.9 20.9	2222222 200000 200000	119.6 119.6 119.6 119.6	
129 127 126.5 126	123 123 122 121 121	119.5 119.5 116.5 115.5	115 114.5 113.5 113.5 113.5	113.5 113 112.5 112.5 112.5
17 18 19 20 21	22 2 2 3 2 2 4 2 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	1 4 12 14 15 16 16 16 16 16 16 16 16 16 16 16 16 16	4 4 4 4 4 0 11 5 5 4 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5

AL I GNMENTS

	PRELIMINARY, PRT; 127 AA.	00 (TrEMBLrel. 15, Created)		25, Last	Onconase variant rapLR1 precursor.	Rana pipiens (Northern leopard frog).	Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,	hia; Anura; Neobatrachia; Ranoidea;		FROM N. A.	ver;	MEDLINE=20330357; PubMed=10871370;	, Le SY., Newton D.L., Maizel J.V. Jr., Rybak S.M.;	xic ribonuclease	3' UTR of unusual length and structure.";	Nucleic Acids Res. 28:2375-2382(2000).	EMBL; AF165133; AAF76935.1;	35; A39035.	069; 1ONC.	GO; GO:0003676; F:nucleic acid binding; IEA.	GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.	InterPro; IPR001427; RNaseA.	Pfam; PF00074; rnaseA; 1.	ProDom; PD000535; RNaseA; 1.	00092; RNAse Pc; 1.	PROSITE; PS00127; RNASE PANCREATIC; 1.	1	1 23 POTENTIAL.	127 AA; 14491 MW; B8511DC5407AB69B CRC64;	100.0%; Score 578; DB 13; Length 127;	100.0%; Pred. No. 3.5e-59;	Conservative 0;
LT 1 V8	Q918V8 Q918V8;	01OCT-2000	01OCT-2000	01-OCT-2003	Onconase var	Rana pipiens	Eukaryota; M	Amphibia; Ba	NCBI_TaxID=8404;	SECUENCE FROM N.A.	TISSUE=Liver;	MEDLINE=2033	Chen SL.,	"A gender-sp	3' UTR of un	Nucleic Acid	EMBL; AF1651	PIR; A39035; A39035.	HSSP; P22069; 10NC.	GO; GO:00036	GO; GO:00045	InterPro; IP	Pfam; PF0007	ProDom; PD00	SMART; SM000	PROSITE; PS0	Signal.	SIGNAL	SEQUENCE 1	Query Match	Best Local Similarity	Matches 104;
RESULT 0918V8	A D	DŢ	텀	I	DΕ	SO	8	8	XO NA	RP	RC	RX	RA	RT	RT	RL	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	X	F	Š	ð	Be	Ma

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1 QDWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT 60

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; TYPE: PRT
ORGANISM: Artificial Sequence
; FRATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Rana pipiens
OTHER INFORMATION: ribonuclease with Met at position 1 and Gln2Ser
; OTHER INFORMATION: substitution (recombinant Met (-1) RaPLR1 Q1S)
US-09-948-191A-13
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	4;
	Gaps
105;	9;
Length	Indels
B 10;	32;
Score 285.5; DB 10;	15; Mismatches 32;
47.18;	•
ilarity	; Conservative
cch sl sim	56;
Query Match	Matches

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Search completed: May 11, 2004, 14:39:23 Job time : 38.1719 secs

62 TTRFQLNTCTRTSITPRPCPYSSRTEINYICVKCENQYPVHFAGIGRCP 110

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GENERAL INFORMATION:

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2 NWATFQQKHIKTPIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINLNVLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Description of Artificial Sequence:Rana OTHER INFORMATION: catesbeiana ribonuclease with Met22Leu and OTHER INFORMATION: Met57Leu substitutions (recombinant RaCOR1 OTHER INFORMATION: Met22Leu Met57Leu)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 110,
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                                                                                                                                                                                                                                                                                                      APPLICANT: Newton, Dianne L.
APPLICANT: The United States of America
APPLICANT: The United States of America
APPLICANT: The United States of the States of the Sapticant: The United States of the Sapticant: The Department of Health and Human Services
TITLE OF INVENTION: Recombinant Anti-Tumor RNase
FILE REFERENCE: 015280-34311005
CURRENT APPLICATION NUMBER: US/09/948,391A
CURRENT FILING DATE: 2002-05-10
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 2090-08-17
NUMBER OF SEQ ID NOS: 43
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APPLICANT: The United States of America
APPLICANT: as represented by The Secretary of the
APPLICANT: Department of Health and Human Services
TITLE OF INVENTION: Recombinant Anti-Tumor RNase
FILE REFERENCE: 015280-343110US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96.5%; Score 585; DB 10;
97.2%; Pred. No. 1.2e-58;
iive 2; Mismatches 1;
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CURRENT FILING DATE: 2002-05-10
PRIOR APPLICATION NUMBER: US 60/079,751
PRIOR FILING DATE: 1998-03-27
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 1999-03-26
PRIOR PILING DATE: 1999-03-16
PRIOR PILING DATE: 1998-03-16
PRIOR FILING DATE: 2000-08-17
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PARENTIN VET. 2.0
SEQ ID NO 13
LENGTH: 105
                                                                                                                                                            ; Sequence 19, Application US/09948391A; Publication No. US20030027311A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 13, Application US/09948391A Publication No. US20030027311A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                           APPLICANT: Rybak, Susanna M. APPLICANT: Newton, Dianne L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Rybak, Susanna M.
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Matches 106; Conservative
                                                                                                                          US-09-948-391A-19
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APPLICANT:
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APPLICANT: RYBAK, SUSANNA M.

APPLICANT: SUBLEMBER, DAVID M.

APPLICANT: GOLDENBERG, DAVID M.

APPLICANT: GOLDENBERG, DAVID M.

APPLICANT: HWION, DIANNE L.

TITLE OF INVENTION: IMMUNOCONUGATES OF TOXINS DIRECTED AGAINST MALIGNANT

TITLE OF INVENTION: LAMOUNOCONUGATES OF TOXINS DIRECTED AGAINST MALIGNANT

TITLE OF INVENTION: LAMOUNOCONUGATES OF TOXINS DIRECTED AGAINST MALIGNANT

FILE REFERENCE: 018733/1059

CURRENT APPLICATION NUMBER: US/09/961,400

CURRENT APPLICATION NUMBER: 09/622,613

PRIOR FILING DATE: 2000-08-17

PRIOR FILING DATE: 1999-03-26

PRIOR FILING DATE: 1999-03-26

PRIOR FILING DATE: 1998-03-26

NUMBER OF SEQ ID NOS: 43

SOFTWARE: PATENTIN VEY: 2.1

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APPLICANT: RYBAK, SUSANNA M.

APPLICANT: GOLDENBERG, DAVID M.

APPLICANT: GOLDENBERG, DAVID M.

APPLICANT: GOLDENBERG, DAVID M.

APPLICANT: GOLDENBERG, DAVID M.

TITLE OF INVENTION: CELLS

TITLE OF INVENTION: CELLS

FILE REPERENCE: 018733/1059

CURRENT APPLICATION NUMBER: US/09/961,400

CURRENT FILING DATE: 2001-09-25

PRIOR APPLICATION NUMBER: PCT/US99/06641

PRIOR PELLOATION NUMBER: PCT/US99/06641

PRIOR PELLOATION NUMBER: PCT/US99/06641

PRIOR FILING DATE: 1999-03-26

PRIOR FILING DATE: 1999-03-26

NUMBER OF SEQ ID NOS: 43

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Pred. No. 7e-60;
2; Mismatches
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97.3%;
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ORGANISM: Rana catesbeiana
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Best Local Similarity 97.3
Matches 108; Conservative
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Matches 107; Conservative
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US-09-961-400-19
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US-09-961-400-19
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APPLICANT: RYBAK, SUSANNA M.
APPLICANT: RYBAK, SUSANNA M.
APPLICANT: GOLDENBERG, DAVID M.
APPLICANT: NEWTON, DIANNE L.
TITLE OF INVENTION: CELLS
FILE REPERENCE: 018733/1059
FILE REPERENCE: 018733/1059
FURNENT APPLICATION NUMBER: U9/09/961,400
CURRENT APPLICATION NUMBER: 09/622,613
PRIOR APPLICATION NUMBER: P0/622,613
PRIOR FILING DATE: 2000-09-17
PRIOR FILING DATE: P099-03-26
PRIOR FILING DATE: 1999-03-26
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                      MSNWATFQQKHIINTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNV
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                                                                                    LSTTREQLNTCTRTSITPRPCPYSSRTEINYICVKCENQYPVHFAGIGRCP 111
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98.3%; Score 596; DB 10; Length 111;
Best Local Similarity 97.3%; Pred. No. 6.6e-60;
Matches 108; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                 Sequence 21, Application US/09948391A
Publication No. US20030027311A1
GENERAL INFORMATION:
APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: The United States of America
APPLICANT: The United States of America
APPLICANT: Department of Health and Human Services
TITLE OF INVENTION: Recombinant Anti-Tumor Rhase
FILE REFERENCE: 015260-343110US
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 21, Application US/09961400 Publication No. US20030124131A1 GENERAL INFORMATION:
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ORGANISM: Artificial Seguence
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APPLICANT: Rybak, Susanna M.
APPLICANT: Rybak, Susanna M.
APPLICANT: The United States of America
APPLICANT: The United States of America
APPLICANT: The United States of America
APPLICANT: as represented by The Secretary of the
APPLICANT: as represented by The Secretary of the
APPLICANT: Department of Health and Human Services
TITLE OF INVENTION: Recombinant Anti-Tumor RNase
FILE REFERENCE: 015280-343110US
CURRENT FILING DATE: 2002-05-10
PRIOR APPLICATION NUMBER: US 60/079,751
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 1999-03-26
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PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 2000-08-17
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PATENTIN VOET: 2.0
                                                                                                                                                                                                                                                                                             Score 596; DB 10;
Pred. No. 6.6e-60;
2; Mismatches 1;
PRIOR APPLICATION NUMBER: 60/079,751
PRIOR FILING DATE: 1998-03-26
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 21
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Best Local Similarity 97.33
Matches 108; Conservative
                                                                                                                                                                                TYPE: PRT
ORGANISM: Rana catesbeiana
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Sequence 15, Application US/09961400
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APPLICANT: Newton, Dianne L.
APPLICANT: The United States of America
APPLICANT: as represented by The Secretary of the
APPLICANT: Department of Health and Human Services
TITLE OF INVENTION: Recombinant Anti-Tumor RNase
FILE REFERENCE: 015280-3431100S
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100.0%; Pred. No. 1.8e-60;
iive 0; Mismatches 0;
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PRIOR APPLICATION NUMBER: US 60/079,751
PRIOR PILING DATE: 1999-03-27
PRIOR PILING DATE: 1999-03-26
PRIOR APPLICATION NUMBER: WO PCT/US99/06641
PRIOR PILING DATE: 1999-03-26
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 2000-08-17
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PATENTIN VET. 2.0
PRIOR FILING DATE: 2000-08-17
PRIOR APPLICATION NUMBER: PCT/US99/06641
PRIOR FILING DATE: 1999-03-26
PRIOR APPLICATION NUMBER: 60/079,751
PRIOR FILING DATE: 1998-03-26
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver. 2.1
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ORGANISM: Artificial Sequence
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ORGANISM: Rana catesbeiana
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                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
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                                                                                                                                                                                                                                                             US-09-961-400-24
                                                                                                                                                                                           LENGTH: 110
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Best Local &
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RESULT 7 US-09-961-400-15

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Publication No. US20030124131A1

GENERAL INFORMATION:

APPLICANT: RYBAK, SUSANNA M.

APPLICANT: RYBAK, SUSANNA M.

APPLICANT: RUBANNION: INMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT

TITLE OF INVENTION: INMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT

TITLE OF INVENTION: UNUMBER: US/09/961,400

CURRENT APPLICATION NUMBER: 09/622,613

PRIOR FILING DATE: 2000-09-17

PRIOR PAPLICATION NUMBER: 09/622,613

PRIOR FILING DATE: 1999-03-26

PRIOR FILING DATE: 1999-03-26

PRIOR FILING DATE: 1999-03-26

PRIOR FILING DATE: 1999-03-26

NUMBER OF SEQ ID NOS: 43

SOFTWARE PATENTIN VOY: 2.1
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13.09-948-391A-17
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APPLICANT: The United States of America
APPLICANT: as represented by The Secretary of the
APPLICANT: Department of Health and Human Services
TITLE OF INVENTION: Recombinant Anti-Tumor RNase
FILE REFERENCE: 015200-343110US
CURRENT APPLICATION NUMBER: US/09/948,391A
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Pred. No. 6.6e-60;
0; Mismatches 2;
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PRIOR FILING DATE: 1998-03-27
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: WO PCT/US99/06641
PRIOR APPLICATION NUMBER: WS 09/622,613
PRIOR FILING DATE: 2000-08-17
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn Ver. 2.0
LENGTH: 111
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Publication No. US20030027311A1
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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Best Local Similarity
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RESULT 4
US-09-948-391A-24
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US-09-961-400-24
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Sequence 26, Application US/09961400

Sublication No. USZ0030124131A1

GENERAL INFORMATION:

APPLICANT: RYBAK, SUSANA M.

APPLICANT: NEWTON: DIANUE L.

TITLE OF INVENTION: INMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT

TITLE OF INVENTION: UNMER: US/09/961,400

CURRENT APPLICATION NUMBER: US/09/25

FILE REFERENCE: 018733/1059

CURRENT FILING DATE: 2000-08-17

FRIOR APPLICATION NUMBER: POT/US99/06641

FRIOR APPLICATION NUMBER: EVT/US99/06641

FRIOR FILING DATE: 1999-03-26

NUMBER OF SEQ ID NOS: 43

SOFTWARE: PATENTING DATE: 1998-03-26

NUMBER OF SEQ ID NOS: 43

SOFTWARE: PATENTIN VET: 2.1
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APPLICANT: GOLDENBERG, DAVID M.
APPLICANT: GOLDENBERG, DAVID M.
THILE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
TITLE OF INVENTION: CELLS
FILE REPERENCE: 018733/1059
CURRENT APPLICATION NUMBER: US/09/961,400
CURRENT PILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: 09/622,613
PRIOR APPLICATION NUMBER: 09/622,613
PRIOR APPLICATION NUMBER: 60/079-751
PRIOR APPLICATION NUMBER: 60/079,751
PRIOR FILING DATE: 1999-03-26
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PALCHING DATE: 1998-03-26
NUMBER OF SEQ ID NOS: 43
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1 MSNWATFQQKHIINTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNV 60
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Publication No. US20030124131A1
GENERAL INFORMATION:
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; ORGANISM: Rana catesbeiana
US-09-961-400-17
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Matches 111; Conservative
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LENGTH: 111
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                                                                                                            1 MSNWATFQQKHIINTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNV 60
                                                                                                                                                2 SNWATFQQKHIINTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNVL 61
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APPLICANT: RYBAK, SUSANNA M.
APPLICANT: GOLDENBERG, DAVID M.
APPLICANT: GOLDENBERG, DAVID M.
TITLE OF INVENTION: IMMUNCONUTGATES OF TOXINS DIRECTED AGAINST MALIGNANT
TITLE OF INVENTION: CELLS
FILE REFERENCE: 018733/1059
CURRENT FILLING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: 09/622,613
                                                          Gaps
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OTHER INFORMATION: catesbeiana ribonuclease with Gln1Ser substitution
OTHER INFORMATION: (recombinant RaCOR1 Q1S)
                                                                                                                                                                                                                            61 LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
                                                                                                                                                                                                                                                                  61 LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
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  Length 111;
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                                                          1; Indels
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JAPPLICANT: Nybak, Susanna M.

APPLICANT: Newton, Dianne L.

APPLICANT: The United States of America
APPLICANT: The United States of America
APPLICANT: The United States of America
APPLICANT: Bepartment of Health and Human Services
TITLE OF INVENTION: Recombinant Anti-Tumor RNase
TITLE OF INVENTION: Recombinant Anti-Tumor RNase
CURRENT APPLICATION NUMBER: US/09/948,391A
CURRENT FILING DATE: 1998-03-510
PRIOR FILING DATE: 1998-03-27
PRIOR FILING DATE: 1998-03-26

PRIOR FILING DATE: 1999-03-6641
PRIOR FILING DATE: 1999-03-66

PRIOR FILING DATE: 1999-03-66

PRIOR FILING DATE: 2000-08-17

NUMBER OF SEQ ID NOS: 43

SOFTWARE: PatentIN Ver. 2.0

SEQ ID NO 24
Score 602; DB 10;
Pred. No. 1.4e-60;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 24, Application US/09948391A, Publication No. US20030027311A1, GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 24, Application US/09961400
; Publication No. US20030124131A1
; GENERAL INFORMATION:
99.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 100.
Matches 110; Conservative
  Query Match
Best Local Similarity 99.1
Matches 110; Conservative
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(without alignments)
807.135 Million cell updates/sec
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| cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl
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	Description	Sequence		Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
		1														
SUMMARIES		US-09-948-391A-26	US-09-961-400-26	US-09-961-400-17	JS-09-948-391A-24	US-09-961-400-24	US-09-948-391A-15	US-09-961-400-15	US-09-948-391A-17	JS-09-948-391A-21	JS-09-961-400-21	US-09-948-391A-22	JS-09-961-400-22	JS-09-961-400-19	JS-09-948-391A-19	JS-09-948-391A-13
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	% Query Match Length DB	111	111	111	110	110	110	110	111	111	111	117	117	110	110	105
	% Query Match	100.0	100.0	99.3	99.2	99.2	98.5	98.5	98.3	98.3	98.3	98.3	98.3	97.5	96.5	47.1
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US-09-961-400-13 US-09-948-391A-6 US-09-961-400-6 US-09-948-391A-11 US-09-961-400-11	US-09-961-400-9 US-10-153-882-2 US-09-961-400-2 US-09-948-391A-28	US-09-961-400-28 US-09-948-391A-2 US-09-961-400-8 US-09-986-119-1	US-09-918-887-1 US-09-948-391A-4 US-09-961-400-4 US-09-948-391A-8	US-09-948-391A-9 US-10-461-713-53 US-09-986-119-3 US-09-918-887-3 US-10-016-447-2	US-10-037-417-103 US-10-016-248-89 US-10-074-978A-139 US-10-074-978A-141 US-10-661-713-52 US-09-9731-872-254 US-09-876-997-254 US-09-981-286A-8
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ALIGNMENTS

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US-09-948-391A-26

Sequence 26, Application US/09948391A
Publication No. US20030027311A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Newton, Dianne L.
APPLICANT: The United States of America
APPLICANT: Department of Health and Human Services
TITLE OF INVENTION: Recombinant Anti-Tumor RNase
TITLE OF INVENTION NUMBER: US/09/948,391A
TITLE OF INVENTION NUMBER: US/09/948,391A
CURRENT APPLICATION NUMBER: US/09/948,391A
CURRENT APPLICATION NUMBER: US/09/948,391A
CURRENT APPLICATION NUMBER: WO PCT/US99/06641
PRIOR FILING DATE: 1999-03-26
PRIOR APPLICATION NUMBER: WO 9/622,613
PRIOR APPLICATION NUMBER: WO 9/622,613
PRIOR APPLICATION NUMBER: WO 9/622,613
PRIOR APPLICATION NUMBER: WO 9/622,613
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PRIOR APPLICATION NUMBER: WO 9/622,6
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54 ---GVINLNVLSTTRFQLNTCTRTSITPRP-CPYSSRTETNYICVKCEN--QYPVHFAGI 107
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Tragulina,
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20 170 BRAIN-TYPE RIBONUCLEASE RIBONUCLEASE.
170 AA; 18832 MW; AB6CE7B1E5549AAO CRC64;</pre>
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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MEDLINE=21347458; PubMed=11453981;

Breukelman H.J., Jekel P.A., Dubois J.Y., Mulder P.P.M.F.A.,

Warmels H.W., Beintema J.J.,

"Secretory ribonucleases in the primitive ruminant chevrotain

"Secretory ribonucleases in the primitive ruminant chevrotain

Eur. J. Biochem. 268:3890-3897(2001).

-i. SINTIARITY: BELONGS TO THE PANCKEATIC RIBONUCLEASE FAMILY.

HSSP: PO0656; 1129; CAC24723.1;

HSSP: PO0656; 1129.
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                                                                                                                                                                               Brain-type ribonuclease ribonuclease precursor (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GO; GO:0004519; F:endonuclease activity; IEA.
GO; GO:0016787; F:hydrolase activity; IEA.
GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
InterPro; IPR001427; RNaseA.
                                                                                                                   (TrEMBLrel. 17, Last sequence update) (TrEMBLrel. 24, Last annotation update)
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                                    170 AA
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PRINTS; PR00794; RIBONUCLEASE.
ProDom, PD000535; RNaseA; 1.
SMART; SM0092; RNASe Pc; 1.
PROSITE; PS00127; RNASE PANCREATIC; 1.
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STRAIN=NMRI;
MEDLINE=22493143; PubMed=12548285;
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                              PRELIMINARY;
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Hooper L.V., Stappenbeck T.S., Hong C.V., Gordon J.I., "Angiogenins: a new class of microbicidal proteins involved in innate immunity.";
                                                                                                                                                                                                                                                                                                                        34 CKRVNTFIISSATTVKAIC---TGVINLNV-LSTTRFQLNTCTRTSITP-RPCPYSSRTE
                                                                                                                                                                                                                                                      21.1%; Score 127.5; DB 11; Length 144; 38.2%; Pred. No. 9.4e-07; tive 13; Mismatches 29; Indels 5;
                                                  Nat. Immunol. 4:269-273(2003).
BMBL; AX219970; AA062354.1; -.
GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0004522; F:pancreatic ribonuclease activity; IEA
                                                                                                                InterPro; IPRO(1427; RNSSEA.
Pfam; PF00074; rnaseA; 1.
PRINTS; PR00794; RIBONUCLEASE.
ProDom; PD000532; RNSSEA; 1.
SMART; SM0092; RNASE Pc; 1.
PROSITE; PS00127; RNASE PanCREATIC; 1.
SEQUENCE 144 AA; 16554 MW; 09808807C00224C1 CRC64;
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122 FRYIVIACEDGWPVHF 137
                                                                                                                                                                                                                                                                                       29; Conservative
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24 QDWDTFQKKHLIDTKKVKCDVEMKKALF----DCKKTNTFIFARPRVQALCKNIKDNIN 79
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"The identification of two novel ligands of the FGF receptor by a yeast screening method and their activity in Xenopus development."; Cell 83:621-630(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Cranīata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                              60 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
                                                                                                                                                                                                                              DB 13; Length 128;
                                                                                                                                                                                                                            35.5%; Score 214.5; DB 13; Length 38.4%; Pred. No. 8.2e-17; ative 20; Mismatches 40; Indels
GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
InterPro; IPR001427; RNaseA.
Pfam; PO0074; rnaseA; 1.
ProDom; PD000535; RNaseA; 1.
PROSTIE; PS00127; RNASE_PANCREATIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
Kinoshita N., Kirschner M.W.;
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AFIS9166; AAD41901.1; -.
HSSP; P00656; 1LSQ.
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GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
InterPro; IPR001427; RNaseA.
PFam; PF00074; rnaseA; 1.
                                                                                                                                            1 23 POTENTIAL.
24 128 RC-RNASEG RIBONUCLEASE.
128 AA; 14804 MW; AFEBFD67D266C7C2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Prodom; PD000535; RNaseA; 1.
PROSITE; PS00127; RNASE PANCREATIC; 1.
SEQUENCE 169 AA; 18891 MW; D969F3E43B3CE1B8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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MEDLINE=96069863; PubMed=7585965;
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Best Local Similarity 39.5.,
Best Local 44; Conservative
                                                                                                                                                                                                                                                                      43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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Best Local Similarity
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                                                                                                                                                                                     SEQUENCE
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                                                                                                                              Signal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 ONWAIFQQKHIINI-PIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGV-INLN 59
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Amphibia, Batrachia, Anura, Neobatrachia, Ranoidea, Ranidae, Rana
                                                                                                                                          RC-RNase3 ribonuclease precursor.
Rana catesbeiana (Bull frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                        Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana
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TISSUB-Liver;
MEDLINE-20512555; PubMed=11058105;
Liao Y.D., Huang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.C.;
"Purification and cloning of cytotoxic ribonucleases from Rana catesbeiana (bullfrog).";
Nucleic Acids Res. 28:4097-4104 (2000).
EMBL; AF242554; AAG31440.2;
HSSP; P22069; 10NC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36.9%; Score 223.5; DB 13; Length 128; 40.2%; Pred. No. 7.5e-18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   GO, GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
InterPro; IRRO147; RNaseA.
ProDom; PF00074; rnaseA; 1.
ProDom; PD000535; RNaseA, 1.
PROSIIE; PS00127; RNASE_PANCREATIC; 1.
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01-0CT-2001 (TrEMBLrel. 18, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                               01-0CT-2001 (TrEMBLrel. 16, Created)
01-0CT-2001 (TrEMBLrel. 18, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
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                                            128 AA
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1-OCT-2003 (TrEMBLrel. 25, Last a
RC-RNase6 ribonuclease precursor.
Rana catesbeiana (Bull frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14517 MW;
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128
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128 AA;
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                                                                                                                                                                                                                              NCBI_TaxID=8400;
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                                                                  Q9DFY7;
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    RESULT 11
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2 ONWALFQOKHII--NTPIICN-TILDNNIYIVGGOCKRVNTFI-ISSATTVKAICTGVIN 57 28 QNINAFMEKHIVKEGAETNCNQTIKDRNIRF-KNNCKFRNTFIHDTNGKKVKEMCAGIVK 86 8; Gaps 58 LN-VLSTTRFQLNTCTRISITPRP.-CPYSSRTETNYICVKCENQYPVHFAG 106

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Length 169;

Indels

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RESULT 14

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InterPro, IPR001427; RNaseA.
Pfam; PF00074; rnaseA; 1.
ProDom; P0000535; RNaseA; 1.
PROSITE; PS00127; RNASE PANCREATIC; 1.
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128 AA; 14839 MW;
                                                                           14724 MW;
                                                                                                          1 Similarity 42.5 48; Conservative
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128
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Matches 44; Conserv
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SIGNAL
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Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
NCBI_TaxID=8404;
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Amphibia, Batrachia, Anura, Neobatrachia, Ranoidea, Ranidae, Rana
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                                                                                                                                                                                                                                                                                                                                                                                                                                               80 VLTTSEFYLSDC---NVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 127
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                                                                                                                                                                                                                                                                                                                                            45.2%; Score 273.5; DB 13; Length 127; 48.6%; Pred. No. 1.3e-23; tive 16; Mismatches 32; Indels 9;
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Liao Y.D., Huang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.C.
"Purification and cloning of cytotoxic ribonucleases from Rana
catesbeiana (bullfrog).";
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Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AF242555, A20141.2; -.
EMBL, IKVZ, 28-UUJ-02.
GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
                                                                                                                                                                                            Lião Y.-D., Wang S.-C.;
"Rana pipiens onconase genomic DNA.";
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                            POTENTIAL. 953F90D351CFEEF3 CRC64;
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Last annotation update)
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Last annotation update)
                       127 AA.
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                                             Created)
                                                                                                Rana pipiens (Northern leopard frog)
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                       PRT;
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Rana catesbeiana (Bull frog).
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SEQUENCE 127 AA; 14469 MW;
                                          01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2002 (TrEMBLrel. 20, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                 54; Conservative
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                       PRELIMINARY;
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                                                                             Onconase precursor
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SEQUENCE FROM N.A.
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SIGNAL
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                                                                                                                                                                                                         2 QNWATFQQKHIINT-PIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NLN 59
                                                                                                                                                                                                                                             24 QDWATFKKKHILDTWDVDCDNLMPTSLF----DCKDKNTFIYSLPGPVKALCRGVIFSAD 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P.-C., Wang S.-C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24 QNWETFQKKHLTDTRDVKCDAEMKKALF----DCKQKNTFIYARPGRVQALCKNIIVSKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 ONWAIFQOKHIINT-PIICNTILDNNIYIVGGQCKRVNIFIISSATTVKAICTGVI-NLN
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                                                                                                                                                    10; Gaps
                                                                                                                                                                                                                                                                                                                   60 VLSTTRFQLNTCTRTSITPR-PCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
                                                                                                                                                                                                                                                                                                                                            Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
NCBI_TaxID=8400;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDINE-20512555; PubMed=11058105;
Liao Y.D., Huang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.C.,
"Purification and cloning of cytotoxic ribonucleases from Rana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
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                                                                                                    Length 129;
                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C Submitted (ANG-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AF24253; AAG31439.1; --
PDB; 1M58; 09-JAN-03.
GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0004222; F:pancreatic ribonuclease activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               989719CF52053ECC CRC64;
                                               826A62882B10ABDA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RC-RNASE2 RIBONUCLEASE
                      RC-RNASE4 RIBONUCLEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01.MAR-2001 (TrEMBLrel. 16, Last sequence update) 1-007-2003 (TrEMBLrel. 25, Last annotation update) RC-RNase2 ribonuclesse precursor. Rana catesbeiana (Bull frog)
                                                                                               40.2%; Score 243; DB 13; I
42.5%; Pred. No. 4.3e-20;
Live 25; Mismatches 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              37.3%; Score 225.5; DB 1 39.3%; Pred. No. 4.4e-18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           128 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00074; rnaseA; 1.
ProDom; PD000535; RNaseA; 1.
PROSITE; PS00127; RNASE_PANCREATIC; 1.
POTENTIAL
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P11916; 1BC4.
                                                                                                                                                                                                                           132 AA;
                                                                                                                                                                                                                                                                                        Best Local Similarity
Matches 72; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mu.
Local Sim.
54;
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                                                                                                                                                             Signal.
SIGNAL
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Q918V8;
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HSSF;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C., Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AF288642; AAG30414.2; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 ONWATFOOKHIINTPII-CNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINLNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                            MEDLINE=21539506; PubMed=11683320;
MEDLINE=21539506; PubMed=11683320;
Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
Rapid diversification of RNase A superfamily ribonuclease from the bullfrog, Rana catesbelana.";
J. Mol. Evol. 53:31-38(2001);
EMBL. APS1208; ARX30254.1; -.
                                                                                                                                                                                                              Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
NCBI_TaxID=8400;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordaľa, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Neobatrachia, Ranoidea, Ranidae, Rana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=20512555; PubMed=11058105; Liao Y.D., Huang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.C.; Warification and cloning of cytotoxic ribonucleases from Rana catesbeiana (bullfrog).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 13; Length 132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 444.5; DB 13; Length
Pred. No. 3e-43;
8; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95D61760F729868E CRC64;
                                                                                                         01-UUN-2001 (TrEMBLrel. 17, Created)
01-UUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2001 (TrEMBLrel. 16, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-OCT-2003 (TrEMBLrel. 12, Last annotation update)
RC-RNasel. ribonuclease precursor.
Rana catesbeiana (Bull frog).
                                                                           132 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  132 AA
                                                                                                                                                                          RNase A-type ribonuclease rc204 precursor.
Rana catesbeiana (Bull frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART; SM00092; RNASE PC; 1.
PROSITE; PS00127; RNASE_PANCREATIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic Acids Res. 28:4097-4104(2000).
                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 22 Pv
132 AA; 14704 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001427; RNaseA.
Pfam; PF00074; rnaseA; 1.
ProDom; PD000535; RNaseA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                73.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 P11916; 1BC4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rissum=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                          098SM1;
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                                                                       Q98SM1
                                                                                                                                                                                                                                                                                                                                                                                                                                              HSSP;
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                              RESULT 5
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                                                                                                                                                                                                                                                                                                                                                                                                                               59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chen S.-L., Le S.-Y., Newton D.L., Maizel J.V. Jr., Rybak S.M.;
"A gender-specific mRNA encoding a cytotoxic ribonuclease contains a 3' UTR of unuaval length and structure.";
Nucleic Acids Res. 28:2375-2382(2000).
EMBL; AF165133; AAF76935.1; -..
PIR; A39035; A39035.
HSSP; P22069; JONC.
GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
InterPro; IPR001427; RNaseA.
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                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
0nconase variant rapLR1 precursor.
Rana pipiens (Northern leopard frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 13; Length 127;
                                                                                                                                                                                                                                                                                                       Length 132;
                                                                                                                                                                                                                                                                                                                                                     Indels
GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
InterPro; IPR001427; RNaseA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                          132 RC-RNASEL1 RIBONUCLEASE.
14625 MW; D8D9A517452FBE53 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     127 AA; 14491 MW; B8511DC5407AB69B CRC64;
                                                                                                                                                                                                                                                                                               61.5%; Score 372; DB 13; I
64.9%; Pred. No. 6.5e-35;
tive 10; Mismatches 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    45.9%; Score 277.5; DB 13;
48.6%; Pred. No. 4.6e-24;
tive 16; Mismatches 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              127 AA
                                                                                                                                                                                                   POTENTIAL.
                                                                     Pfam; PF00074; rnaseA; 1.
Probom; PD000535; RNaseA; 1.
SMART; SM0092; RNAse Pc; 1.
PROSITE; PS00127; RNASE PANCREATIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam, PF00074; rnaseA; 1.
ProDom; PD000535; RNaseA; 1.
SMART; SM00092; RNAse_Pc; 1.
PROSTIE; PS00127; RNASE_PANCREATIC; 1.
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                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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23 QNWATFQQKHITNTSSINCSNIMMNSLYIVGGQCKKVNTFIASSATTVKGICSGVTDKKV 82
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 QNWATFQQKHIINTPII-CNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINLNV
Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;

"Rapid diversification of RNase A superfamily ribonuclease from the bullfrog, Rana catesbelana.";

J. Mol. Evol. 53:31-38 (2001).

EMBL; AF351210; AAK30256.1; -.

HSSP; P19156; 1B64.

GO; GO:0003676; F:nucleic acid binding; IEA.

GO; GO:0003676; F:nucleic acid binding; IEA.

GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.

InterPro; IPR01427; RNaseA.

Probow, PD000535; RNaseA.; 1.

SMART; SM00092; RNase Ec; 1.

PROSITE; PS00127; RNASE_PANCREATIC; 1.
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"Rapid diversification of RNase A superfamily ribonuclease from the
bullfrog, Rana catesbeiana.",
J. Mol. Evol. 53:31-38(2001).
BMBL; APS51211; AAK30257.1; -.
HSSP; P11916; 1BC4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        stana catesbelana (Bull Irog).
Bukaryota; Metazoa; Chorala, Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 LSTTRFQLNTCTRISITPRPCPYSSRIETNYICVKCENQYPVHFAGIGRCP 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      83 LSSTKFOLDICTRIFITPRPCPYSSRTETNYICVKCENOYPVHFAGIGOCP 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 13; Length 133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 13; Length 133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 78.4%; Score 474.5; DB 13; Length 77.5%; Pred. No. 1.1e-46; Live 12; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
InterPro; IPR001427; RNaseA.
Pfam; PF00074; rnaseA; 1.
Propor; PD000535; RNaseA; 1.
SMART; SM00092; RNASe Pc; 1.
PROSITE; PS00127; RNASE Pc; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C8785B236B26E54E CRC64;
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133 AA; 14590 MW; 8B40B9A94FA5B943 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
10-CT-2003 (TrEMBLrel. 25, Last annotation update)
10-CT-2003 (TrEMBLrel. 25, Last annotation update)
10-CT-2003 (TrEMBLrel. 25, Last annotation update)
10-CT-2004 (Trema
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       77.3%; Score 467.5; DB 13; 75.7%; Pred. No. 6.7e-46; Live 14; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          133 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=21539506; PubMed=11683320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22 P
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mes 86; Conservative
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01-JUN-2001
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Q98SL8;
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Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
"Rapid diversification of RNase A superfamily ribonuclease from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
RNase A-type ribonuclease rc212 precursor.
Rana catesbeina (Bull frog).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
RNase A-Pype ribonuclease rc203 precursor (RC-RNase7 precursor).
Rana catesbeiana (Bull frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
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Pred. No. 9.7e-48;
6; Mismatches 12; Indels 1;
                                                LSTTRFQLNTCTRTSITPRPCPYSSRTEINYICVKCENQYPVHFAGIGRCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Liver;
Liao Y.-D., Tang P.-C., Jeng J.-T.;
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF351207; AAK30253.1; -.
EMBL; AF359578; AAL87036.1; -.
HSSP; P11916; 1BC4.
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GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
InterPro; IPR001427; RNaseA.
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23 132 RC-RNASE7.
132 RA; 14412 MW; 131A745187978687 CRC64;
                                                                                                                                                                                                                                                                                                                      132 AA.
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PROSITE; PS00127; RNASE PANCREATIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                           (TrEMBLrel. 17, Created)
                                                                                                                                                                                                                                                                                                                      PRT;
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SEQUENCE FROM N.A.
MEDLINE=21539506; PubMed=11683320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               bullfrog, Rana catesbeiana.";
J. Mol. Evol. 53:31-38(2001).
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82.7%;
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                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00074; rnaseA; 1
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=8400;
                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                         83
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Matches

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C98SL9
ID 098S.
AC 098S.
DT 01-0
DT 01-0
DE RNas
OC Euka
OC Amph.
OX NCBI
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RR (21)
RR SEQUI
RR MEDLI

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Q861y5 colobus gue Q9tvc0 sus scrofa Q9bdc2 antilocapra Q8vd94 berylmys bo Q8vd88 rattus norv Q9bh14 antilocapra

balaena mys

O7yrj5 tursiops tr Q8k2t2 mus musculu Q8c6g3 mus musculu

Q861y4 trachypithe Q84d92 rattus exul Q861y2 pygathrix r Q861y2 pygathrix a Q861y1 pygathrix a Q84d89 rattus norv Q86663 mus musculu Q95ne6 bubalus bub Q86764 mus musculu Q84055 berylmys bo Q80764 mus musculu Q80765 tragulus ja Q9bec2 tragulus ja Q9bec3 tragulus ja Q9bec3 tragulus ja Q9bec3 tragulus ja Q86364 attus tiom Q86305 lagothrix l

Q8sq06 ateles geof Q9bec3 tragulus ja Q8sq08 saimiri sci saguinus oe

29tv30

Run on:

Title:

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2 ONWATFOOKHIINTPII-CNTILDNNIYIVGGOCKRVNTFIISSATTVKAICTGVINLNV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23 QNWATFQQKHITNTSSINCNTIMDNNIYIVGGQCKGVNTFIISSATTVKAICTGVINMNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIJINE-21239506; PubMed=11683320;
MEDIJINE-21239506; PubMed=11683320;
Rosenberg H.F., Zhao Y.-D., Dyer K.D.;
"Rapid diversification of RNase A superfamily ribonuclease from the bullfroy, Rana catesbelana.";
J. Mol. Evol. 5:31-38(2001).
EMBL; AR351209; AAK30255.1;
HSSP; P11916; 1864.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OTT-2003 (TrEMBLrel. 25, Last annotation update)
RNase A-type ribonuclease rc208 precursor.
Rana catesbejana (Bull frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 13; Length 133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91.7%; Score 554.5; DB 13; Length 92.8%; Pred. No. 6.6e-56; ive 2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
InterPro; IPR001427; RNaseA.
Pfam; PF00074; rnaseA.
Probon; PD000535; RNaseA. 1.
SMART; SM00092; RNASE PC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22 POTENTIAL.
14628 MW; 87FCF122C3499E02 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART; SM00092; RNASE PC; 1.
PROSITE; PS00127; RNASE_PANCREATIC; 1.
                                          Q9BDC2
Q8VD94
Q8VD88
Q9BH14
                                                                                                     Q7YRJ5
Q8K2T2
Q8C6G3
Q8C1Y4
Q8VD92
Q8VD92
                                                                                                                                                                                         2861Y1
Q861Y1
Q8VD89
Q8C663
Q9SNE6
Q8C7E4
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Q8SQ06
Q9BEC3
Q8SQ08
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              Q861Y5
Q9TVC0
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Q9BDB9
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Best Local Similarity 92.8
Matches 103; Conservative
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133 AA;
                                                        NCBI_TaxID=8400;
                                                                                                                                                                                                                                                                                                              108.5
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118.5
116.5
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SIGNAL
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Q9bec1 tragulus ja
Q80z85 mus musculu
Q80xs4 mus musculu
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                                                                                                7, 2004, 21:29:10 ; Search time 31.566 Seconds (without alignments) 1109.503 Million cell updates/sec
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Q9df78 n
Q9i8v8 n
Q8uvx5 n
Q9dfy6 n
Q9dfy8 n
Q9dfy7 n
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Q98s19
Q98s18
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            GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                 1017041 seqs, 315518202 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                    OM protein - protein search, using sw model
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Q80Z85
Q80XS4
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Q98SL9
Q98SL8
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Q9DF78
Q9I8V8
Q8UVX5
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sp_virus:*
sp_vertebrate:*
sp_unclassified:*
                                                                                                                                                                                                                                       Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                               sp archea: *
sp bacteria: *
sp fung: *
sp numan: *
sp invertebrate: *
sp mammal: *
sp mammal: *
sp organelle: *
sp phage: *
sp phage: *
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Maximum DB seq length: 200000000
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Match Length
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128
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483.5
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225.8
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Result No. ij

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Q9BEC1

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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19 POTENTIAL.
170 BRAIN-TYPE RIBONUCLEASE RIBONUCLEASE.
18832 MW; AB6CE7E1E5549AAO CRC64;
                                                                                                     Tragulus javanicus (Lesser Malay chevrotain).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Tragulina;
                                                                                                                                                                                                                                                                              (Tragulus javanicus).";
Eur. J. Biochem. 268:3890-3897(2001).
-!- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
EMBL; AJ271299; CAC24723.1; -.
ENSP; PO0656; 1LSQ.
                                                                                                                                                                                                                MEDLINE=21347458; PubMed=11453981;
Brenkelman H.J., Jekel P.A., Dubois J.Y., Mulder P.P.M.F.A., Warmels H.W., Beintema J.J., In the primitive ruminant chevrotain "Secretory ribonucleases in the primitive ruminant chevrotain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 170;
                      01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Brain-type ribonuclease ribonuclease precursor (Fragment).
                                                                                                                                                                                                                                                                                                                                                           GO; GO:0004519; F:endonuclease activity; IEA.
GO; GO:0016789; F:hydroclase activity; IEA.
GO; GO:0004522; F:pancreatic ribonuclease activity; IEA
INTERPRO; IPR001427; RNaseA.
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Last sequence update)
Last annotation update)
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170 AA
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PROSITE; PS00127; RNASE PANCREATIC; 1.
Endonuclease; Hydrolase; Nuclease; Signal.
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SQUENCE FROM N.A.
STRAIN=NWRI;
MEDLINE=22493143; PubMed=12548285;
PRT;
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PRINTS; PR00794; RIBONUCLEASE.
ProDom; PD000535; RNaseA; 1.
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01-JUN-2003 (TrEMBLrel. 24,
01-OCT-2003 (TrEMBLrel. 25,
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PRELIMINARY;
                                                                                                                                                       Tragulidae; Tragulus.
NCBI_TaxID=9849;
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170 AA;
                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                           RNASE B.
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                 Q9BEC1;
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 O9BEC1
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                                                                                                                                                                                                                                                                                                                                                                                                         34 CKRVNTFIISSATTVKAIC---TGVINMNV-LSTTRFQLNTCTRTSITP-RPCPYSSRTE
Hooper L.V., Stappenbeck T.S., Hong C.V., Gordon J.I., Magiogenins: a new class of microbicidal proteins involved in innate
                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                               5,
                                                                                                                                                                                                                                                                                                                       Query Match 21.2%; Score 128.5; DB 11; Length 144; Best Local Similarity 38.2%; Pred. No. 4.6e-07; Matches 29; Conservative 13; Mismatches 29; Indels 5;
                                                         Mat. Immunol. 4:269-273 (2003).

Mat. Immunol. 4:269-273 (2003).

EMBL, AY219870; AAO62354.1; -.

EMBL, AY219870; AAO62354.1; -.

EMBL, AY219870; AAO62354.1; -.

GO, GO:0004522; F:panoreatic acid binding; IEA.

InterPro; IPR001427; RNaseA.

ERAM; FR00794; RIBONUCLEASE.

ProDom; PD000535; RNaseA; 1.

SWART; SM00092; RNASeP; 1.

SWART; SM00092; RNASEP; 1.

SRART; SW00092; RNASE PANCREATIC; 1.

SRART; SW00092; RNASE PANCREATIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Search completed: May 11, 2004, 14:36:30 Job time : 36.6606 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                89 TNYICVKCENQYPVHF 104
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|22 FRYIVIACEDGWPVHF 137
                                              immunity.";
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FRL2 protein.
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                                                                                                          SEQUENCE
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                                                                                   SIGNAL
                                                                                                                                                                                                                                                                                                                Q9W73B
                                                                         Signal
                                                                                               CHAIN
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Q9W738
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Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF242556; AAG31442.2; -.
HSSP; P22069; IONC.
                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                               RC-RNase3 ribonuclease precursor.
Rana catesboiana (Bull frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae, Rana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
NCBI_TaxID=8400;
                                                                                                                                                                        MEDLINE=20512555; PubMed=11058105; Liao Y.D., Huang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.C., "Purification and cloning of cytotoxic ribonucleases from Rana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81 LSRDAFLLPQCDRIKL---PCHYKLSSSTNTICITCVNQLPIHFAGVGSCP 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIINE=20512555; PubMed=11058105;
Liao Y.D., Huang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.C., "Purification and cloning of cytotoxic ribonucleases from Rana catesbeiana (bullfrog).":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
                                                                                                                                                                                                                                                                                                                                                                                                                     6
                                                                                                                                                                                                                                                                                                                                                                                              DB 13; Length 128;
                                                                                                                                                                                                                                                                                                                                                                                             ch 36.6%; Score 221.5; DB 13; Length
| Similarity 40.5%; Pred. No. 5.7e-18;
45; Conservative 18; Mismatches 39; Indels
                                                                                                                                                                                                                                                             GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
InterPro; IPR001427; NaseA.
Pfam; PF00074; rnaseA; 1.
Probom; PD000535; RnaseA; 1.
                                                                                                                                                                                                                                                                                                                                                          24 128 RC-RNASE3 RIBONUCLEASE.
128 AA; 14517 MW; 2B14986082E0587D CRC64;
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(TrEMBLrel. 18, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
                                           (TrEMBLrel. 16, Created)
(TrEMBLrel. 18, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
                        128 AA.
                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
                                                                                                                                                                                                               catesbeiana (bullfrog).";
Nuclea Acids Res. 28:4097-4104 (2000).
EMBL; AR242554; AAG31440.2; --
HSSP; P22069; 10NC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28:4097-4104(2000).
                       PRT;
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                       PRELIMINARY;
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Best Local Similarity
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                                                                                                                             NCBI_TaxID=8400;
                                                                                                                                                                 TISSUE=Liver;
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                                                         01-OCT-2001
                                                                 01-OCT-2003
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                                             01-MAR-2001
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                      Q9DFY7
                                                                                                                                                                                                                                                                                                                                     Signal
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RESULT 11
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3 NWATFQQKHIINT-PIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGV-INMNV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25 DWDTFQKKHLTDTKKVKCDVEMKKALF---DCKKTNTFIFARPPRVQALCKNIKDNTNV 80
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"The identification of two novel ligands of the FGF receptor by a yeast screening method and their activity in Xenopus development.";
Cell 83:621-630(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Xenopus laevis (African clawed frog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81 LSRDVFYLPQCNRKKL---PCHYRLDGSTNTICLTCMKELPIHFAGVGKCP 128
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                                                                                                                                                                                                                                                                                                                              35.1%; Score 212.5; DB 13; Length 128; 38.7%; Pred. No. 6.4e-17; vative 19; Mismatches 40; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP
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GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
InterPro; IPR001427; RNaseA.
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Kinoshita N., Kirschner M.W.;
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AFIS9166; AAD41901.1; -.
HSSP; P00656; 1LSQ.
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GO; GO:0004522; F:pancreatic ribonuclease activity; IEA
InterPro; IFR01427; RNaseA.
Pfam; PF00074; rnaseA: 1.
                                                                                                                                                                                                              1 23 POTENTIAL.
24 128 RC-RNASEG RIBONUCLEASE.
128 AA; 14804 MW; AFEBFD67D266C7C2 CRC64;
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PROSITE; PS00127; RNASE PANCREATIC; 1.
SEQUENCE 169 AA; 18891 MW; D969F3E43B3CE1B8 CRC64;
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Last annotation update)
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38.7%; Pred. No. 2e-10;
iive 10; Mismatches 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                169 AA
                                                                                       Pfam; PF00074; rnaseA; 1.
ProDom; PD000535; RNaseA; 1.
PROSITE; PS00127; RNASE_PANCREATIC; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                   43; Conservative
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                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
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InterPro, IPR001427; RNaseA.
Pfam; PF00074; rnaseA; 1.
ProDom; PD000535; RNaseA; 1.
PROSITE; PS00127; RNASE_PANCREATIC; 1.
                                                                                                                                                                                                                                                                                                                                                 48; Conservative
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128 AA;
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SIGNAL
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EMBL; AF242555; AAG31441.2; -.
PDB; IKVZ; 28-JUL-02.
GO; GO:0004576; F:nucleic acid binding; IEA.
GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
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Amphibia, Batrachia, Anura, Neobatrachia, Ranoidea, Ranidae, Rana.
NCBI_TaxID=8404;
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Rana catebbeiana (Bull frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
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Liao Y.D., Huang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.C.;
"Purification and cloning of cytotoxic ribonucleases from Rana
catesbeiana (bullfrog).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 45.0%; Score 272.5; DB 13; Length 127; Best Local Similarity 49.1%; Pred. No. 6.3e-24; Matches 54; Conservative 15; Mismatches 32; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases. EMBL, AF332139; AAL54383.1; -. PIR, A39035, A39035. Go.0003676; F.nucleic acid binding; IEA. GO, GO:0004222; F.nucleic ribonuclease activity; IEA. InterPro; IPR01427; RNaseA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIGNAL 1 23 POTENTIAL.
SEQUENCE 127 AA; 14469 MW; 953F90D351CFEEF3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-WAR-2001 (TrEMBLrel. 16, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                  127 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM00092; RNASE PC; 1.
PROSITE; PS00127; RNASE_PANCREATIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Liao Y.-D., Wang S.-C.; "Rana pipiens onconase genomic DNA.";
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                                                                                                                                                                                                                                                                                         Rana pipiens (Northern leopard frog).
                                                                                                                                 Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00074; rnaseA; 1.
ProDom; PD000535; RNaseA; 1.
                                                                                                                          01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2002 (TrEMBLrel. 20, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                  PRELIMINARY;
                                                                                                                                                                                                                                Onconase precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9DFY6;
                                                                  Q8UVX5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9DFY6
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      RESULT 8
                                    Q8UVX5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    D9DFY6
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Iniao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AR242553; AAG31439.1; --
PDB; 1M58; 09-JAN-03
GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0004522; F:spanceatic ribonuclease activity; IEA.
InterPro; IPR001427; RNaseA.
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                                                                                                                                                                   Indels 10; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RC-RNase2 ribonuclease precursor.
Rana catesbeiana (Bull frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana
                                                                                                                                                                                                                                                                                                                                                                           61 LSTTRFQLNTCTRTSITPR-PCPYSSRTETNYICVKCENOYPVHFAGIGRCP 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=20512555; PubMed=11058105;
Liao Y.D., Huang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.C.;
"Purification and cloning of cytotoxic ribonucleases from Rana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81 LSTDEFYLSDCNRIKL---PCHYKLKKSSNTICITCENKLPVHFVAVEECP 128
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                                                                                                                 Length 129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RC-RNASE2 RIBONUCLEASE.
989719CF52053ECC CRC64;
                                                        129 AA; 14724 MW; 826A62882B10ABDA CRC64;
                          RC-RNASE4 RIBONUCLEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                      30;
                                                                                                           39.8%; Score 241; DB 13;
42.9%; Pred. No. 3.1e-20;
tive 24; Mismatches 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  128 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00074; rnaseA; 1.
ProDom; PD000535; RNaseA; 1.
PROSITE; PS00127; RNASE PANCKEATIC; 1.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        catesbeiana (bullfrog).";
Nucleic Acids Res. 28:4097-4104(2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14839 MW;
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HSSP; P11916; 1BC4.
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                                                                                                                                     SEQUENCE
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                                                                                                 Signal.
SIGNAL
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SIGNAL
                                                                                                                                                                                                                                                                                                                                                              09I8V8;
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                                                                                                                         CHAIN
                                                                                                                                                                                      Matches
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DR RICH BRANCH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C., Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AF288642; AAG30414.2; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 NWATFOOKHIINTFII-CNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                              MEDLINE=21539506; PubMed=11683320;
REDLINE=21539506; PubMed=11683320;
Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
Rapid diversification of RNase A superfamily ribonuclease from the bullfrog, Rana catesbeiana.";
J. Mol. Evol. 53:31-38(2001).
EMBL; AF551208; AAK30254.1; -.
HSSP; P11916; 1BC4.
                                                                                                        RNase A-type ribonuclease rc204 precursor.

Rnan catesbeiana (Bull frog).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.

NCBI_TaxID=8400;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rana catesbeiana (Bull frog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Neobatrachia, Ranoidea, Ranidae, Rana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-Liver;
MEDLINE=20512555; PubMed=11058105;
Liao Y.D., Huang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.C.;
"Purification and cloning of cytotoxic ribonucleases from Rana catesbeina (bullfrog)";
Nucleic Acids Res. 28:4097-4104(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                  1;
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                                                                                                                                                                                                                                                                                                                                                                                                                          DB 13; Length 132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STTRPOLXXXTRTFITSRPCPYSSTKETNKICVKCENEYPVHFAGIGKC 132
                                                                                                                                                                                                                                                                                                                                                                                                                        73.2%; Score 443.5; DB 13; Length 78.0%; Pred. No. 7.3e-44; ive 7; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                   GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
95D61760F729868E CRC64;
                                                                     01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2001 (TrEMBLrel. 16, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                               132 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                132 AA
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ProDom; PD000535; RNaseA; 1.
SMART; SM0092; RNASe Pc; 1.
PROSITE; PS00127; RNASE PANCREATIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RC-RNaseL1 ribonuclease precursor.
                                                                                                                                                                                                                                                                                                                                                                                     22 PC
14704 MW;
                                                                                                                                                                                                                                                                                                            InterPro; IPR001427; RNaseA.
                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 73.2
Best Local Similarity 78.0
Matches 85; Conservative
                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                 132 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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01-MAR-2001
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                                                                                                                                                                                                                                                                                                                                                                           Signal.
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                                              Q98SM1
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Q9DF78
                       RESULT 5
                                 Q98SM1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23 NWAKFKEKHITSTSSIDCNTIMDKAIYIVGGKCKERNTFIISSEDNVKAICSGVSPDRKE 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C. TLSUBLELLOYE;
X. MEDLINELLOYE;
X. MEDLINELLOYE;
Y. MEDLINELLOYE;
Y. MEDLINELLOYE;
Y. Le S.-Y., Newton D.L., Maizel J.V. Jr., Rybak S.M.;
X. Chen S.-L., Le S.-Y., Newton D.L., Maizel J.V. Jr., Rybak S.M.;
X. Then S.-L., Le S.-Y., Newton D.L., Maizel J.V. Jr., Rybak S.M.;
X. Then S.-L., Le S.-Y., Newton D.L., Maizel J.V. Jr., Rybak S.M.;
X. Then S. Le musual length and structure.";
X. Mucleic Acids Res. 28:2375-2382(2000).
X. Nucleic Acids Res. 28:2375-2382(2000).
X. RHSP; AS9053; AS9035.
X. ARPI, AS9053; AS9035.
X. Massello S. Rinasea, I.
X. Massello S. Rinasea, I.
X. Makri; SM00092; RNAse_Pc; I.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 NWATFOOKHIINT-PIICNTIMDNNIYIVGGOCKRVNTFIISSATTVKAICTGVI-NMNV
                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rana pipiens (Northern leopard frog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Neobatrachia, Ranoidea, Ranidae, Rana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LSTISFKLNTCIRDSIIPRPCPYHPSPDNNKICVKCEKOLPVHFVGIGKC 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        45.6%; Score 276.5; DB 13; Length 127; 49.1%; Pred. No. 2.2e-24; ive 15; Mismatches 32; Indels 9;
                                                                                                                                                                                                                                                                                                                     Length 132;
                                                                                                                                                                                                                                                                                                                                                                         27; Indels
GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
InterPro; IPR001427; RNaseA.
                                                                                                                                                                                                           POTENTIAL.
RC-RNASEL1 RIBONUCLEASE.
D8D9A517452FBE53 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     127 AA; 14491 MW; B8511DC5407AB69B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           update)
                                                                                                                                                                                                                                                                                                                  Score 371; DB 13;
Pred. No. 2.1e-35;
                                                                                                                                                                                                                                                                                                                                                                   9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  127
                                                                                                 Probom; PD000535; RNaeeA; 1.
SMART; SM00092; RNASe Pc; 1.
PROSITE; PS00127; RNASE PANCREATIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00092; RNASe_Pc; 1.
PROSITE; PS00127; RNASE_PANCREATIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Onconase variant rapLR1 precursor.
                                                                                                                                                                                                                                                               14625 MW;
                                                                                                                                                                                                                                                                                                                     61.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-2000 (TrEMBLrel, 15, 01-OCT-2000 (TrEMBLrel, 15,
                                                                                                                                                                                                                                                                                                                                                                      72; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               54; Conservative
                                                                            Pfam; PF00074; rnaseA; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (TrEMBLrel. (TrEMBLrel.
                                                                                                                                                                                                                                      22 1
132 AA;
                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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RESULT 2

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Q98SM2

us-09-961-400-26.rspt

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Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
"Rapid diversification of RNase A superfamily ribonuclease from the full freey Rana catesbelana";
Julifreey, Rana catesbelana";
J. Mol. Evol. 53:31-38(2001).

BMBL; AF351210; AAK30256.1;
BMBL; AF351210; AAK30256.1;
RSP; P11916; IBG4.
GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
RO; GO:0004522; F:naseA.
InterPro; IPR001427; RNaseA.
RP Fam; FR00074; rnaseA; 1.
RP Probom; PD000535; RNaseA; 1.
RP PROSITE; PS00127; RNASE_PC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                133
                                                                                                                                                                                                                                                   POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-2001 (TrEMBLrel. 17, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                   1 22 P
133 AA; 14615 MW;
                                                                                                                                                                                                                                                                                                   78.1%;
78.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                      86; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=8400;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84;
                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                                                    Signal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  098SL8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 WATFOOKHIINTPII-CNTIMDNNIYIVGGOCKRVNTFIISSATTVKAICTGVINMNVLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                  MEDLINE=21339506; PubMed=11683320; Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.; Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.; Rarialy diversification of Rhase A superfamily ribonuclease from the bullfrog, Rana catesbeian "; J. Mol. Evol. 53:31-38(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordařa; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Rana.
NCBI_TaxID=8400;
                                                                                                                                                                            01-JUN 2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last amnotation update)
RNase A-type ribonuclease rc203 precursor (RC-RNase7 precursor).
RNase A-type ribonuclease rc203 precursor (RC-RNase7 precursor).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1;
                           STIRFOLNICIRISITPRPCPYSSRIETNYICVKCENQYPVHFAGIGRCP 111
                                       STTRFQLNTCTRTSITPRPCPYSSRTENNYICVKCENQYPVHFAGIGRCP 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 13; Length 132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     85 PTRFQLDTCTRTSITPRPCPYSSKKETNKICVKCENQLPVHFAGIGKC 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lido Y.-D., Tang P.-C., Jeng J.-T.;
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF351207; AAK302531; -.
HSSP; P11916; 1BC4.
GO; GO:0003676; P:nucleic acid binding; IEA.
GO; GO:0004522; F:nuclearic ribonuclease activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RC-RNASE7.
131A745187978687 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-0TN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          79.6%; Score 482.5; DB 1:
84.3%; Pred. No. 2.1e-48;
tive 5; Mismatches 11
                                                                                                                                              132 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RNase A-type ribonuclease rc212 precursor.
Rana catesbeiana (Bull frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SM00092; RNASe_Pc; 1.
PROSITE; PS00127; RNASE_PANCREATIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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SEQUENCE FROM N.A.
MEDLINE=21539506; PubMed=11683320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23 132 R
132 AA; 14412 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ProDom; PD000535; RNaseA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 84.3
Matches 91; Conservative
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                                                                                                                                                PRELIMINARY;
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132
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                                                                                                                                                                                                                                                                                                     NCBI_TaxID=8400;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Liver;
                            62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63
                                                                                                                                                                Q98SM2;
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RESULT 3

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                                                                                                                                                                                            24 NWATFQQKHITNTSSINCSNIMNNSLYIVGGQCKKVNTFIASSATTVKGICSGVIDKKVL 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 NWATFQOKHIINTPII-CNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNVL 61
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                                                                                                                                                               3 NWATFOOKHIINTPII-CNTIMDNNIYIVGGOCKRVNTFIISSATTVKAICTGVINMNVL
                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=21539506; PubMed=11683320;
Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
"Rapid diversification of RNase A superfamily ribonuclease from the bullifrog, Rana catesbeiana.";
J. Mol. Evol. 5:31-38(2001).
BMBL, AF351211; AAK30257.1;
HSSP; P11916; 1BG4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 капа сасевретала (вил1 frog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Neobatrachia, Ranoidea, Ranidae, Rana
                                                                                                                                                                                                                                                                                                             1;
                                                                                                                                                                                                                                                                             STTRFQLNTCTRISITPRPCPYSSRTEINYICVKCENQYPVHFAGIGRCP 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STTRFQLNTCTRISITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
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                                                    Length 133;
                                                 $; Score 473.5; DB 13; Length
b; Pred. No. 2.3e-47;
11; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 77.0%; Score 466.5; DB 13; Length
76.4%; Pred. No. 1.5e-46;
Live 13; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GO; GO:0005676; F:nucleic acid binding; IEA.
GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
InterPro; IPR001427; RNaseA.
InterPro; IPR001427; RNaseA.
Propon; PD00074; rNaseA; 1.
SMART; SM00092; RNASE PC; 1.
PROSITE; PS00127; RNASE PC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 22 POTENTIAL.
133 AA; 14590 MW; 8B40B9A94FA5B943 CRC64;
C8785B236B26E54E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
1-OCT-2003 (TrEMBLrel. 25, Last annotation update)
RNase A-type ribonuclease rc218 precursor.
Rana catesbeiana (Bull frog).
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Q7yrj6 balaena mys
Q8vd94 berylmys bo
Q9bdc2 antilocapra
Q8vd88 rattus norv
Q861y4 trachypithe
Q9bh14 antilocapra
Q861y2 pygathrix r
Q861y2 pygathrix r
Q861y2 pygathrix s
Q861y2 pygathrix a
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Q8623 mus musculu
Q8623 mus musculu
Q8vd92 rattus norv
Q95ne6 bubalus bub
Q87ne6 bubalus in
Q8vd95 berylmys bo
Q9bdb9 tragulus ja
Q8vd95 lagothrix l
Q8vd95 lagothrix l
Q8vd96 atagulus ja
Q8vd96 atagulus ja
Q8vd06 ateles geof
Q9bec2 tragulus ja
Q8sq06 ateles geof

Q7YRJ6 Q8VD94 Q8VD8 Q8VD8 Q8VD8 Q861Y3 Q861Y3 Q861Y3 Q861Y3 Q861Y3 Q8C6G3 Q8CCG3 Q8CCG3 Q8CCG3 Q8CCB4 Q8CCB5 Q8CCB6 Q8CCB6 Q8CDB9 Q8CCB6 Q8CDB9 Q8CCB6 Q8CDB9 Q8CCB6 Q8CDB9 Q8CCB6 Q8CDB9 Q8CCB6 Q8CDB9 Q8CCB6 Q8CDB9 Q8CCB6 Q8CDB9 Q8CCB6 Q8CDB9 Q8CCB6 Q8CCB

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Q9dfy6 rana catesb
Q9dfy6 rana catesb
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Copyright (c) 1993 - 2004 Compugen Ltd.
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No.
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ALIGNMENTS

56	KESULT I Q98SM0							
	098SM0	PRELIMINARY;	PRT;	133 AA.				
	098SM0;							
	01-JUN-2001		Creat					
	01-00N-2001			sequence update)				
	01-OCT-2003	(TrEMBLrel. 25, Last	, Last ann	annotation update)	е)			
	RNase A-type	RNase A-type ribonuclease rc208 precursor	rc208 prec	ursor.				
	Rana catesb	Rana catesbeiana (Bull frog).	g).					
	Eukaryota; 1	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;	ta; Crania	ta; Vertebrat	a; Euteleostomi;	ostomi		
	Amphibia; Ba	Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea;	; Neobatra	chia: Ranoide		e: Rar		
	NCBI TaxID=8400;	8400;						
	Ξ							
	SEQUENCE FROM N.A.	OM N.A.						
	MEDLINE=215	MEDLINE=21539506; PubMed=11683320;	1683320;					
	Rosenberg H.	Rosenberg H.F., Zhang J., Liao YD., Dyer K.D.;	Liao YD.	, Dyer K.D.;				
	"Rapid diver	rsification of 1	RNase A su	perfamily rib	onuclease	from	the	
	bullfrog, Ra	bullfrog, Rana catesbeiana.	· =.					
	J. Mol. Evo.	J. Mol. Evol. 53:31-38(2001).	1).					
	EMBL; AF3512	EMBL; AF351209; AAK30255.1;						
	HSSP; P11916	P11916; 1BC4.						
	GO; GO:00036	GO:0003676; F:nucleic acid binding; IEA.	acid bindi	ng; IEA.				
	GO; GO:0004E	GO:0004522; F:pancreatic ribonuclease activity;	ic ribonuc	lease activit	y; IEA.			
	InterPro; 11	InterPro; IPR001427; RNaseA.	Α.					
	Pfam; PF0007	Pfam; PF00074; rnaseA; 1.						
	ProDom; PD0(ProDom; PD000535; RNaseA; 1	1.					
	SMART; SM00(092; RNAse Pc;	1.					
	PROSITE; PS(PROSITE; PS00127; RNASE PANCREATIC; 1.	NCREATIC;	۲.				
	Signal.							
	SIGNAL	1 22	POTENTIAL.	AL.				
	SEQUENCE 1	133 AA; 14628 MW;		87FCF122C3499E02 C	CRC64;			
	Query Match	01.7%;		Score 555.5; DB 13;	Length 133;	133;		
	Matches 104;	vat	0	Fred. NO. 0.36-5/; ; Mismatches 5;	Indels	1;	Gaps	Н
	3 NWA	NWATEQOKHIINTPII - CNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINNNVL	CNTIMDNNIY	IVGGQCKRVNTFI	ISSATTVKA	ICTGVI	NMNAL	61
							=	
	24 NW2	NWATFQQKHITNTSSINCNTIMDNNIYIVGGQCKGVNTFIISSATTVKAICTGVINMNVL	CNTIMDNNIY	INGGOCKGNNTFI	ISSATTVKA	ICTGVI	NMINAL	83

Q9BEC1 Q80Z85 Q80XS4

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      <1 19 POTENTIAL.
20 170 BRAIN-TYPE RIBONUCLEASE RIBONUCLEASE.
170 AA; 18832 MW; AB6CE7E1E5549AAO CRC64;
                                                                                 Tragulus javanicus (Lesser Malay chevrotain).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Traguliaa; Tragulidae; Tragulus.
                                                                                                                                                                                                                                                                                      (Tragulus javanicus).";
Eur. d. Biochem. 268:3897(2001).
Eur. -i. SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
EMBL; AJ271<u>12</u>99; CAC24723.1; -.
                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE=21347458; PubMed=11453981;
Breukelman H.J., Jekel P.A., Dubois J.Y., Mulder P.P.M.F.A.,
Breukelman H.W., Beintema J.J.;
"Secretory ribonucleases in the primitive ruminant chevrotain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ch 21.8%; Score 131; DB 6; Length 170; Similarity 33.1%; Pred. No. 2.8e-07; 41; Conservative 17; Mismatches 46; Indels
                            01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Brain-type ribonuclease ribonuclease precursor (Fragment).
RNASE B.
                                                                                                                                                                                                                                                                                                                                                               GO; GO:0004519; F:endomuclease activity; IEA.
GO; GO:0016787; F:hydrolase activity; IEA.
GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
InterPro; IPR001427; RNaseA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-UUN-2003 (TrEMBLrel. 24, Created)
01-UUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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170 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00074; rnaseA; 1.

PRINTS; PR00794; RIBONUCLEASE.

ProDom; P0000535; RNaseA; 1.

SMORY: SM00092; RNAse Pc; 1.

PROSITE; PS00127; RNASE PANCREATIC; 1.

Endonuclease; Hydrolase; Nuclease; Signal.
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MEDLINE-22493143; PubMed=12548285;
PRT;
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 PRELIMINARY;
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Best Local Similarity
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62 CKDVNTFIHGTKKNIRALCGKKGSPYGENFRISNSPFQITTCTHSRGSPWPPCGYRAFKD 121
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Gooper L.V., Stappenbeck T.S., Hong C.V., Gordon J.I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                   Immuniary.

Nat. Immunol. 4:269-273(2000).

R EMBL, AV219870; AA062354.1; -.

R GO; GO:0003676; F:nucleic acid binding; IEA.

R GO; GO:0003672; F:pancreatic ribonuclease activity; IEA.

R GO; GO:0004822; F:pancreatic ribonuclease activity; IEA.

R R GO; GO:0004822; F:pancreatic ribonuclease activity; IEA.

R R GO; GO:0004822; F:pancreatic ribonuclease activity; IEA.

R R GO:0000362; F:NaseA.

R PRINTS; PR00074; RIBONUCLEASE.

DR PRODOM; PR00052; RNASE P.1.

DR RAMAR; SM00092; RNASE PANCREATIC; 1.

PROSITE; PS00127; RNASE PANCREATIC; 1.

THE ROSITE; PS00127; RNASE PANCREATIC; 1.
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Rana catesbeiana (Bull frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
NCBI_TaxID=8400;
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01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
RC-RNase6 ribonuclease precursor.
Rana catesbeiana (Bull frog).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Barrachia; Anura; Neobatrachia; Ranidae; Rana.
NCBI_TAXID=8400;
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MEDLINE-20512555; PubMed=11058105;
Liao X.D., Huang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.C.;
"Purification and cloning of cytotoxic ribonucleases from Rana catesbeiana (bullfrog).";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic Acids Res. 28:4097-4104 (2000).

EMBL; AF245554; AAG31440.2; -.

HSSP; P22069; 10NC.

GO; GO:00037575; F:nucleic acid binding; IEA.

GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.

InterPro; IPR001427; RNaseA.
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                                                                                                                  01-MAR-2001 (TrEMBLrel. 16, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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                                                                 128 AA.
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ProDom; PD000535; RNaseA; 1.
PROSITE; PS00127; RNASE_PANCREATIC; 1.
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                                                              PRELIMINARY;
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MEDIJNE=96069865; PubMed=7585965;
Kinoshita N., Minshull J., Kirschner M.W.;
Kinoshita N., Minshull J., Kirschner M.W.;
"The identification of two novel ligands of the FGF receptor by a yeast screening method and their activity in Xenopus development.";
Cell B3:621-630(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58 N-VLSTTRRQLNTCTRTSITPRP--CPYSSRTETNYICVKCENQYPVHFAG 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       88 TFVISKELLPLIDCLIMGRIARPPNCAYNQTRITGVINITCENNYPVHFAG 138
                                                                                                                                                                                                                                                                                                                                                           6
                                                                                                                                                                                                                                                                                                     35.4%; Score 212.5; DB 13; Length 128; llarity 38.7%; Pred. No. 6.3e-17; Conservative 19; Mismatches 40; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60 LSTTRFQLNTCTRISITPRPCPYSSRIETNYICVKCENQYPVHFAGIGRCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 169;
GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
InterPro; IPR001427; RNaseA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kinoshita N., Kirschner M.W.;
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
InterPro; IPR001427; RNaseA.
                                                                                                                                                                                       1 23 POTENTIAL.
24 128 RC-RNASEG RIBONUCLEASE.
128 AA; 14804 MW, AFEBFD67D266C7C2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00074; rnaseA; 1.
ProDom; PD000535; RNaseA; 1.
PROSITE; PS00127; RNASE PANCREATIC; 1.
SEQUENCE 169 AA; 18891 MW; D969F3B43B3CE1B8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26.3%; Score 158; DB 12
38.7%; Pred. No. 2e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    169 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10; Mismatches
                                                                            Pfam; PF00074; rnaseA; 1.
ProDcm; PD000535; RNaseA; 1.
PROSITE; PS00127; RNASE_PANCREATIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Xenopus laevis (African clawed frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF159166; AAD41901.1; -. HSSP; P00656; 1LSQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NCV-1999 (TrEMBLrel. 12, 01-NCV-1999 (TrEMBLrel. 12, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Xenopodinae; Xenopus.
NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
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InterPro; IPR001427; RNaseA.
Pfam; PF00074; InaseA; 1.
ProDom; PD000535; RNaseA; 1.
PROSITE; PS00127; RNASE_PANCREATIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    catesbeiana (bullfrog)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                   1
24 1;
129 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 44; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                         SEQUENCE
                                                                                                                                                                               Query Match
                                                                                Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9DFY8
                                                                                                                       CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9DFY8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
NCBI_TaxID=8400;
                                                                                                                                                                             Rana pipiens (Northern leopard frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=20512555; PubMed=11058105;
Liao Y.D., Huang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.C.;
"Purification and cloning of cytotoxic ribonucleases from Rana
catesbelana (Dullfrog).";
Nucleic Acids Res. 28:4097-4104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60 LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                81 LTTSEFYLSDC---NVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
45.3%; Score 272.5; DB 13; Length 127;
Best Local Similarity 49.1%; Pred. No. 6.2e-24;
Matches 54; Conservative 15; Mismatches 32; Indels 9;
                                                                                                                                                                                                                                                                                             Liao Y.-D., Wang S.-C.;
"Rana pipiens onconase genomic DNA.";
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF32139; AAL54383.1;
PIR; A39035; A39035.
FOR PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PROBLES PRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIGNAL 1 23 POTENTIAL.
SEQUENCE 127 AA; 14469 MW; 953F90D351CFEEF3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (TrEMBLrel. 16, Created)
(TrEMBLrel. 18, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
                                                                                    20, Created)
20, Last sequence update)
25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               129 AA
                                                127 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SM00092; RNASe_Pc; 1.
PROSITE; PS00127; RNASE_PANCREATIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RC-RNase4 ribonuclease precursor.
Rana catesbeiana (Bull frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00074; rnaseA; 1.
ProDom; PD000535; RNaseA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                  PRELIMINARY;
                                                                                    01-MAR-2002 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                   Onconase precursor
                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                              NCBI_TaxID=8404;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9DFY6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART;
                                                  QBUVX5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 9
Q9DFY6
            RESULT 8
                                  28UVX5
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                                                                                                                                                                                                          2 NWATFQQKHIINT-PIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NMNV 59
                                                                                                                                                                                                                                                   25 DWAJFKKKHLIDIWDVDCDNLMPISLF----DCKDKNIFIYSLPGPVKALCRGVIFSADV 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.; Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF242553; AAG31439.1; -
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                                                                                                                                                            10; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
RC-RNase2 ribonuclease precursor.
Rana catesbeiana (Bull frog).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Raniae; Rana.
                                                                                                                                                                                                                                                                                                                                                           60 LSTIRFQLNICTRISITPR-PCPYSSRIBINYICVKCENQYPVHFAGIGRCP 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=20512555; PubMed=11058105;
Liao Y.D., Huang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.C.;
"Purification and cloning of cytotoxic ribonucleases from Rana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91 LSTDEFYLSDCNRIKL---PCHYKLKKSSNTICITCENKLPVHFVAVBECP 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60 LSTTRFQLNTCTRISITPRPCPYSSRTEINYICVKCENQYPVHFAGIGRCP 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
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                                                                                               / Match 129; Score 241; DB 13; Length 129; Local Similarity 42.9%; Pred. No. 3e-20; Los 48; Conservative 24; Mismatches 30; Indels 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PDB; 1M58; 09-JAN-03.

GO; GO:0003676; F:nucleic acid binding; IEA.

GO; GO:0004522; F:panoreatic ribonuclease activity; IEA.

InterPro; IPR01427; RM3seA.

ProDom; PP00074; rnaseA; 1.

ProDom; PD000535; RNaseA; 1.

PROSIIE; PS00127; RNASE_PANCREATIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
RC-RNASE2 RIBONUCLEASE.
989719CF52053ECC CRC64;
                    RC-RNASE4 RIBONUCLEASE.
826A62882B10ABDA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         37.4%; Score 224.5; DB 1.
39.6%; Pred. No. 2.5e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             39.6%; Pred. w...
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic Acids Res. 28:4097-4104(2000)
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128 AA; 14839 MW;
                                                    14724 MW;
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5,

Gaps

098SM1;

098SM1

RESULT 5

IMS860

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2 NWAIFQOKHIINTPII-CNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NMNV 59
                                                                                                                                                                                                                                                                                                                                                               23 NWAKFKEKHITSTSSIDCNTIMDKAIYIVGGKCKERNTFIISSEDNVKAICSGVSPDRKE 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 NWATFOOKHIINT-PIICHTIMDNNIYIVGGOCKRVNTFIISSATTVKAICTGVI-NMNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-20330357; PubMed=10871370; Chen S.-L., Le S.-Y., Newton D.L., Maizel J.V. Jr., Rybak S.M.; Chen S.-L., Le S.-Y., Newton D.L., Maizel J.V. Jr., Rybak S.M.; "A gender-specific mRNA encoding a cytotoxic ribonuclease contains 3' UTR of unusual length and structure."; Mucleic Acids Res. 28:2375-2382(2000).

EMBL; AF165133; AAF76935.1; -.
PIN; A39035, A39035.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Onconase variant rapLR1 precursor.
Rana pipiens (Northern leopard frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
                                                                                                                                                                                                                                                                                                                                                                                                    60 LSTTRFQLNTCTRTSITPRPCPYSSRTEINYICVKCENQYPVHFAGIGRC 109
                                                                                                                                                                                                                                                                                                                                                                                                                        2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60 LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 127;
                                                                                                                                                                                                                                               DB 13; Length 132;
                                                                                                                                                                                                                                             61.7%; Score 371; DB 13; Length 1
65.5%; Pred. No. 2e-35;
ive 9; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    46.0%; Score 276.5; DB 13; Length
49.1%; Pred. No. 2.1e-24;
ive 15; Mismatches 32; Indels
             GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
InterPro; IPR001427; RNaseA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GO: GO:0003676; F:nucleic acid binding; IEA.
GO: GO:0004522; F:pancreatic ribonuclease activity; IEA.
InterPro; IPR001427; RNaseA.
                                                                                                                                                                                      RC-RNASEL1 RIBONUCLEASE.
D8D9A517452FBE53 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              127 AA; 14491 MW; B8511DC5407AB69B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15, Last sequence update)
25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         127 AA
                                                                                                                                                                        POTENTIAL.
                                                                   Pfam; PF00074; rnaseA; 1.
ProDom; PD000535; RNaseA; 1.
SMART; SM00092; RNASe_Pc; 1.
PROSITE; PS00127; RNASE_PANCREATIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00127; RNASE PANCREATIC; 1.
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                                                                                                                                                                                                          132 AA; 14625 MW;
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ProDcm; PD000535; RNaseA; 1.
SMART; SM00092; RNAse_Pc; 1.
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Best Local Similarity
'... 72; Conservative
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                                                                                                                                                                      21
HSSP; P11916; 1BC4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.; Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AF288642; AAG30414.2; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 NWATFQQKHIINTPII-CNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMAVL
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                                                                                                                                                                                                                                                                                                               Rosenberg H.P., Zhang J., Liao Y.-D., Dyer K.D.;
"Rapid diversification of RNase A superfamily ribonuclease from the bullfrog, Rana catesbeiana.";
J. Mol. Evol. 53:31-38[200].
EMBL; AF351208; AAK30254.1; -.
                                                                                                                     01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
RNase A-type ribonuclease roz04 precursor.
Rana catesbelana (Bull frog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Amphibia, Batrachia, Anura, Neobatrachia, Ranoidea, Raniae, Rana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2001 (TrEMBLrel. 16, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
RC-RNaseL1 ribonuclease precursor.
Rana catesbelana (Bull frog).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=20512555; PubMed=11058105;
Liao Y.D., Huang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.C.,
"Purification and cloning of cytotoxic ribonucleases from Rana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 13; Length 132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 STTRFQLNTCTRISITPRPCPYSSRTEINYICVKCENQYPVHFAGIGRC 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                          HSSP; P11916; 1BC4.
GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0004522; F:pancreatic ribonuclease activity; IEA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            73.8%; Score 443.5; DB 78.0%; Pred. No. 7e-44;
                                                                       132 AA
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Nucleic Acids Res. 28:4097-4104(2000).
                                                                                                       (TrEMBLrel. 17, Created)
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                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=21539506; PubMed=11683320;
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Pfam; PF00074; rnaseA; 1.
ProDom; PD000535; RNaseA; 1.
SWART; SM0092; RNAse Pc; 1.
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                                                                   PRELIMINARY;
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es 85; Conserv
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                                                                                                         01-JUN-2001
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SEQUENCE FROM N.A.
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 WATFOOKHIINTPII-CNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNVLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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"Rapid diversification of RNase A superfamily ribonuclease from the bullfrog, Rana catesbeiana.";
J. Mol. Evol. 53:31-38(2001).
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OT-2003 (TrEMBLrel. 25, Last annotation update)
RNase A-type ribonuclease rc212 precursor.
Rana cateabeiana (Bull frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
NCBL_TaxID=8400;
                                                                                                        01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation produces
RNASE A-type ribonuclease rc203 precursor (RC-RNase7 precursor).
Rana catesbelana (Bull frog).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Rania, NCBI_TAXID=8400;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1;
                       80.3%; Score 482.5; DB 13; Length 132;
84.3%; Pred. No. 2e-48;
iive 5; Mismatches 11; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62 TTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PTRFQLDTCTRTSITPRPCPYSSKKETNKICVKCENQLPVHFAGIGKC 132
           STTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP
                                                                                                                                                                                                                                                                                                              Liao Y.-D., Tang P.-C., Jeng J.-T.;
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF351207; AAK30253.1; -.
EMBL; AF359578; AAL87036.1; -.
                                                                                                                                                                                                                                                                                                                                                             HSSP; P11916; 1BC4.
GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
InterPro; IFR01427; RNaseA.
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: 131A745187978687 CRC64;
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                                                                                        132 AA.
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PROSITE; PS00127; RNASE_PANCREATIC; 1.
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SEQUENCE FROM N.A.
MEDLINE=21539506; PubMed=11683320;
                                                                                        PRT;
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SEQUENCE FROM N.A.
MEDLINE=21539506; PubMed=11683320;
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ProDom; PD000535; RNaseA; 1.
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Q98SL9
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Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
"Rapid diversification of RNase A superfamily ribonuclease from the bullfroy, Rana catesbelana.";
J. Mol. Evol. 53:31-38 (2001).
EMBL; AF351210; AAK30256.1;
HSSP; P19916; 1804.
GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
InterPro; IPR001427; RNaseA.
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
RNase A-type ribonuclease rc218 precursor.
Rna catebbelana (Bull frog).
Eukaryota; Metazoa; Chordeta; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Raniae; Rana.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 133;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ch 78.8%; Score 473.5; DB 13; Length I Similarity 78.2%; Pred. No. 2.2e-47; 86; Conservative 11; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0004522; F:pancreatic ribonuclease activity; IEA
InterPro; IPR001427; RNaseA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 22 POTENTIAL.
133 AA; 14590 MW; 8B40B9A94FA5B943 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                              C8785B236B26E54E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         76.4%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       133
                                                                                                                                                                                                                                                                        Pfam; PF00074; rnaseA; 1.
ProDom; PD000535; RnaseA; 1.
SMART; SM0092; RnAse Pc; 1.
PROSITE; PS00127; RNASE_PANCREATIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SM00092; RNASe_Pc; 1.
PROSITE; PS00127; RNASE_PANCREATIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL
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                                                                                                                                                                                                                                                                                                                                                                                                                       1 22 P
133 AA; 14615 MW;
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ProDom; PD000535; RNaseA; 1.
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84; Conservative
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0861y3 pygathrix r
0861y2 pygathrix b
0861y1 pygathrix a
070x15 tursiops tr
0861y5 colobus gue
0862t2 mus musculu
08663 mus musculu
0804092 rattus exul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9bdb9 tradulus ja
Q8vd84 rattus tiom
Q8sq05 lagothrix l
Q8c663 mus musculu
                                                                              Q9tvc0 sus scrofa
Q8vd88 rattus norv
Q861y4 trachypithe
Q9bh14 antilocapra
                                                                                                                                                                                                                                                                                                                                                                                                 Q8vd89 rattus norv
Q95ne6 bubalus bub
Q8c7e4 mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ogbec3 tragulus ja
Q8sq06 ateles geof
Q9bec2 tragulus ja
Q8sq08 saimiri sci
        7yrj6 balaena mys
Q8vd94 berylmys bo
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                                                        Q9bdc2 antilocapra
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SEQUENCE FROM N.A.

MEDLINE=21539506; PubMed=11683320;

Rosenberg H.F., Zhang J., Liaco Y.-D., Dyer K.D.;

Rosenberg H.F., Zhang J., Liaco Y.-D., Dyer K.D.;

Rapid diversification of RNase A superfamily ribonuclease from the Unifrog, Rana catesbeiana.";

J. Mol. Evol. 53:31-38(2001).

BMBL; AF351209; AAK30255.1;

RSP; P11916; 1BC4.

ROS GO:0003676; F:nucleic acid binding; IEA.

ROS GO:0003676; F:nucleic acid binding; IEA.

ROS GO:000452; F:nasea.

ROS GO:000452; F:nasea.

REMBL; RASO0735; RNasea.

REMBL; SM00092; RNASe_Pc; 1.

REMBL; SM00092; RNASE_PANCREATIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24 NWATFQQKHITNTSSINCNTIMDNNIYIVGGQCKGVNTFIISSATIVKAICTGVINNNVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 NWATFOOKHIINTPII-CHTIMDNNIYIVGGOCKRVNTFIISSATTVKAICTGVINMAVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
NCBI_TaxID=8400;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 92.4%; Score 555.5; DB 13; Length 133; Best Local Similarity 94.5%; Pred. No. 6e-57; Matches 104; Conservative 0; Mismatches 5; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22 POTENTIAL.
14628 MW; 87FCF122C3499E02 CRC64;
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01-UIN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
RNase A-type ribonuclease rc208 precursor.
Rana catesbeiana (Bull frog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALIGNMENTS
                                                                                                                                 Q861Y4
Q9BH14
Q9BH14
Q861Y3
Q861Y2
Q861Y1
Q7YRJ5
Q861Y5
Q861Y5
Q862Y5
Q8603
Q866G3
Q866G3
Q806G3
Q806G3
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Q8VD95
Q9BDB9
Q8VD84
Q8SQ05
Q8C663
Q9TV28
                          Q8VD94
Q9BDC2
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Q8VD88
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Q8SQ06
Q9BEC2
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  \begin{array}{c} \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{L} \\ \mathsf{
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Compugen Ltd.
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                        GenCore version
Copyright (c) 1993 - 2004
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Maximum Match 100%
Listing first 45 summaries
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Q9W738
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sp_plant:*
sp_rodent:*
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sp_vrrtebrate:*
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sp_vrctebrate:*
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Gapop 10.0 , Gapext 0.5
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sp_mammal:*
sp_mhc:*
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sp_bacteria:*
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